

Result No.	Score	Query Match	Length	DB	ID	Description
1	339	100.0	372	6	A84378	A84378 Sequence 14
2	339	100.0	372	6	BD075295	BD075295 Novel met
3	304.4	89.8	339	9	AJ621239	AJ621239 Homo sapi
4	300.6	88.7	339	9	AF035024	AF035024 Homo sapi
5	292.6	86.3	362	9	HSA308463	AJ308463 Homo sapi
6	291.8	86.1	345	9	AB063888	AB063888 Homo sapi
7	291.6	86.0	342	9	H51GVCA	23166 H.sapiens
8	291.6	86.0	437	9	HSE5435	214203 H.sapiens
9	286.6	84.5	342	9	HS4579107	214203 H.sapiens
10	285.6	84.2	398	9	HSE5310	214168 H.sapiens
11	285.4	84.1	345	9	AB067097	AB067097 Homo sapi
12	285.2	84.1	336	9	HS4579114	AJ307911 Homo sapi
13	285.2	84.1	354	9	HSAS300793	AJ300793 Homo sapi
14	284.4	83.9	357	6	AX300024	AX300024 Sequence
15	284	83.8	376	9	AF15111	AF15111 Homo sapi
16	283.8	83.7	354	9	AF063288	AF063288 Homo sapi
17	283.4	83.6	399	9	HS1GXXY7	X55899 H.sapiens
18	283	83.5	363	9	AF062116	AF062116 Homo sapi
19	282.6	83.4	354	9	HS4245291	AJ245291 Homo sapi

20	282.6	83.4	414	9	AF062277	Homo sapi
21	282.6	83.3	351	9	HA245286	Homo sapi
22	282.4	83.3	351	9	HS4245307	Homo sapi
23	282.4	83.3	351	9	HS4579139	Homo sapi
24	282.4	83.3	351	9	HS4579151	Homo sapi
25	282.2	83.2	345	9	AB063830	Homo sapi
26	282	83.2	392	9	HSB5555	214192 H. sapiens r
27	281.8	83.1	351	9	AY530317	Homo sapi
28	281.8	83.1	354	9	AB063813	Homo sapi
29	281.8	83.1	354	9	AB063815	Homo sapi
30	281.4	83.0	360	9	HS4245350	Homo sapi
31	281.4	83.0	360	9	HS4245351	Homo sapi
32	281.2	82.9	357	9	AB627235	Homo sapi
33	281.2	82.9	357	9	AB627243	Homo sapi
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36	280.8	82.8	357	9	AF063287	Homo sapi
37	280.8	82.7	358	9	AF035021	Homo sapi
38	279.6	82.5	357	9	HS457909	Homo sapi
39	279.4	82.4	345	9	AY392931	Homo sapi
40	279	82.4	348	9	HS4245279	Homo sapi
41	278.4	82.1	381	6	BD139667	A novel m
42	278.4	82.1	381	6	AX003755	Sequence
43	278.4	82.1	414	6	AB4376	AB4376 Sequence 14
44	278.4	82.1	414	6	BD075294	Novel met
45	278.4	82.1	1530	6	BD222938	Heteromet

ALIGNMENTS

	RESULT	1			
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	DEFINITION	Sequence 145 from Patent WO9646645.			
	ACCESSION	A84378			
	VERSION	A84378.1	GI:6733301		
	KEYWORDS	.			
	SOURCE	unidentified			
	ORGANISM	unidentified			
	REFERENCE	unclassified.			
	AUTHORS	1 (bases 1 to 372)			
	TITLE	Kufer,P. and Raum,T.			
	JOURNAL	NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND USES THEREOF			
	PATENT	Patent: WO 9846645-A 145 22-OCT-1998;			
	INVENTOR	KUFER PETER (DE); RAUM TOBIAS (DE)			
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	Best Local Similarity	100.0%; Pred. No.9,2e-100; Indels 0; Gaps 0;			
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Oy	61	TTCCTGTGACACTCTTGATTCACTTTGAATGATTAATGCCATGCATGGATCGCCAC	GGCT	120	
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QY	121	CCAGGCAAGGGGCTGAGTGGGTGGCTGACATTATATCATATGATGGAAGTAATTAATCACT	180
Db	121	CCAGGCAAGGGGCTGAGTGGGTGGCTGACATTATATCATATGATGGAAGTAATTAATCACT	180
QY	181	GCAGACTCCGTAAGAGGGCCGATTCACATCTCCAGAGACAATTCACAAGACACGCTGTAT	240
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QY	301	GGCTACTGGGCGCAGGGAAACCTGTGTACCGCTTCCTCA	339
Db	301	GGCTACTGGGCGCAGGGAAACCTGTGTACCGCTTCCTCA	339
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LOCUS			linear
DEFINITION	BD075295		PAT 27-AUG-2002
ACCESSION	BD075295		
VERSION	BD075295.1	GI:22620898	
KEYWORDS	JP 2001519824-A/24.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 372)		
JOURNAL	Kufner, P. and Raum, T.		
COMMENT	Novel method for the production of anti-human antigen receptors and		
	uses thereof		
	Patent: JP 2001519824-A 24 23-OCT-2001;		
	MICROMET AG		
	OS Homo sapiens (human)		
	PN JP 2001519824-A/24		
	PD 23-OCT-2001		
	PF 14-APR-1998 JP 1998543494		
	PR 14-APR-1997 EP 97106109.8		
	PI PETER KUFNER, TOBIAS RAUM		
	PC C07K16/00, C07K16/30, A61K39/395		
	CC Novel method for the production of anti-human antigen CC		
	receptors and uses		
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Db	241	CTGCAATGAAACAGCTTGAGAGCTTGAGGACAACGCTGTATTACTGTGCAAAAAAGAA	300
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Qy	241	CTGCAGAAATGAAACAGCCTTGAGAGCTGAGGACACGGCTGTGATTATCTGTGCGAAAGGAA	300
Db	241	CTGCAGAAATGAAACAGCCTTGAGAGCTGAGGACACGGCTGTGATTATCTGTGCGAAAGGAA	300
Qy	301	GGCTATCTGGGGCCAGGGAAACCTCTGTGATACCGTCTCCCA	339
Db	301	GGCTATCTGGGGCCAGGGAAACCTCTGTGATACCGTCTCCCA	339
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LOCUS	AJ627239	339 bp	mRNA linear PRI 30-JUN-2004
DEFINITION	Homo sapiens partial mRNA for IgD immunoglobulin heavy chain		
ACCESSION	AJ627239	variable region (IGHV3-30 gene), clone T3.3.13.	
VERSION	AJ627239.1	GI:49523851	
KEYWORDS	IGHV3-30 gene; immunoglobulin heavy chain; variable region.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	Dono, M.		
TITLE	Characterization of a novel CD5+ B cell population		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 339)		
AUTHORS	Dono, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-FEB-2004) Dono M., Oncologia Medica C, Istituto Nazionale Ricerca sul Cancro, L.go R. Benzi 10, Italy, 16132, ITALY		
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Qy	62	CCTGTGACGCTCTGATTCACTTTGATGATTAATGACATGCACTGGGTCGCCAGGCTC	121
Db	62	CCTGTGACGCTCTGATTCACTTTGATGATTAATGACATGCACTGGGTCGCCAGGCTC	121
Qy	122	CAGCGAAGGGGCTGAGTGGGTGCGAGTTATATCATATGATGAAGTAAATTAATACTATG	181

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QY 302 GCTACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 339
Db 302 AGACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 339

RESULT 4
AF035024 339 bp mRNA linear PRI 24-SEP-1999
LOCUS AF035024
DEFINITION Homo sapiens clone MCE11H myosin-reactive immunoglobulin heavy chain variable region mRNA, partial cds.
ACCESSION AF035024
VERSION AF035024.1 GI:5921600
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 339)
AUTHORS Wu,X., Liu,B., Van der Werwe,P.L., Kalis,N.N., Berney,S.M. and Young,D.C.
TITLE Myosin-reactive autoantibodies in rheumatic carditis and normal fetus
JOURNAL Clin. Immunol. Immunopathol. 87 (2), 184-192 (1998)
MEDLINE 98277139
PUBMED 9614934
REFERENCE 2 (bases 1 to 339)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-1997) Department of Pathology and Laboratory Medicine, University of Texas Health Science Center, 6431 Fannin, Houston, TX 77030, USA

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Query Match 88.7%; Score 300.6; DB 9; Length 339;
Best Local Similarity 92.9%; Pred. No. 3.6e-87;
Matches 315; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGGTGCAAGCTGCTGAGTCTGGGGAGTCTGTGTAACGCTGGGGGCTCCCTGAGATC 60
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Db 241 CTGCAAAATGAACAGCCTGAGAGTGAAGACACGCGTGTATTAAGTGTGCAAAAAGAA 300
QY 301 GGTACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 339
Db 301 AACTACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 339

RESULT 5
HSA308463 362 bp mRNA linear PRI 06-FEB-2002
LOCUS HSA308463
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV3 gene), clone TEG4.
ACCESSION AJ308463
VERSION AJ308463.1 GI:12734095
KEYWORDS IGHV3 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Jacobin,M.J., Laroche-Traineau,J., Little,M., Keller,A., Peter,K., Welschof,M., Nurdan,A. and Clouet-Sanchez,G.
TITLE Human IgG monoclonal anti-alpha(IIB)beta(3)-binding fragments derived from immunized donors using phage display
JOURNAL J. Immunol. 168 (4), 2035-2045 (2002)
MEDLINE 21681719
PUBMED 11823541
REFERENCE 2 (bases 1 to 362)
AUTHORS Clouet-Sanchez,G.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Clouet-Sanchez G., UMR5533, Cnrs, Hopital Cardiologique, Av de Magellan, 33604 Pessac, FRANCE

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Best Local Similarity 92.8%; Pred. No. 1.5e-84;
Matches 320; Conservative 0; Mismatches 19; Indels 6; Gaps 1;

QY 1 GAGGTGCAAGCTGCTGAGTCTGGGGAGTCTGTGTAACGCTGGGGGCTCCCTGAGATC 60
Db 1 GAGGTGCAAGCTGCTGAGTCTGGGGAGTCTGTGTAACGCTGGGGGCTCCCTGAGATC 60

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QY	181	GCAGACTCCGTGAAAGGGCCGATTCACATCTCCAGAGACAATTCAGAGAACACGGCTGTAT	240
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QY	241	CTGCAATGAAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTAATCTGTGCCGAAAAAG---	297
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QY	339	CTGCAATGAAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTAATCTGTGCCGAAAAAG---	339
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LOCUS	AB063888	345 bp	mRNA	linear	FRI 02-JUL-2002
DEFINITION	Homo sapiens IGH mRNA for immunoglobulin heavy chain VHJ region, partial cds, clone:H238.				
ACCESSION	AB063888				
VERSION	AB063888.1 GI:2166977				

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
1
Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,

TITLE Construction and characterization of antibody libraries: isolation and characterization of monoclonal antibodies

Journal Title
 Journal Reference
 Authors
 Title
 Direct Submission
 Submitted (25-JUN-2001) Yoshihazu Kurosawa, Institute for
 Unpublished
 2 (Pages 1 to 345)
 Kurosawa, Y.

COMMENT
Please visit our web site
URL:<http://www.fujita-hu.ac.jp/immunity/>.

FEATURES	Location/Qualifiers
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gene	1. .345
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CDS	<1. .>345

Query Match	86.1%;	Score 291.8;	DB 9;	Length 345;
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Qy	61	TCTGTGACAGCCTGGATATTCCTTTGATGATTAATGCATGTGACTGGTCCGCGACGCT	120
Db	61	TCTGTGACAGCCTTGTGATTTACCTTTCAGTACGTATGATGATGACTGGTCCGCGACGCT	120
Qy	121	CCAGCGAAAGGGCGTGGAGTGGGTGGCACTTATATATATGATGAGAAATAAATACTAT	180
Db	121	CCAGCGAAAGGGCGTGGAGTGGGTGGCACTTATATATATGATGAGAAATAAATACTAT	180
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Db	241	CTGCAAATGAAACAGCTTGAGACTTGAGACACACGCGTGTATTCTGTGCAAAAGGGCGG	300
Qy	295	AAGGAGGCTTACGTGGGGCCAGGGAAACCTGTGACCCGCTTC	335
Db	301	ACTGGGAGCTACTGGGGCCAGGGAAACCTGTGTCACCGCTTC	341

RESULT 7	HSIGHVCA	LOCUS	DEFINITION
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	H.sapiens (H11)		gene for immunoglobulin heavy chain variable region.

ACCESSION Z31686
VERSION Z31686.1 GI:509782
KEYWORDS immunoglobulin heavy chain; immunoglobulin heavy chain variable region.

ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (Bases 1 to 342)	Riglini M., Marks J.D., Winter G. and Griffiths A.D.	In vitro assembly of hypercoides of antibody chains on the surfaces of phage by renaturation	J. Mol. Biol. 239 (1), 68-78 (1994)

PUBMED REFERENCE	8196048 2 (bases 1 to 342)
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TITLE Direct Submission
JOURNAL Submitted (30-MAR-1994) A.D. Griffiths, MRC Centre for Protein

FEATURES

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 Db 94 AGTGCAGCTGGTGGAGCTCTGGGGGAGAGCTGTGTATCAGCCTGGGAGGCTCCCTAGACTCT 153

62 CCGTGTGAGCCCTGTGATTCACCTTTAGATATGACATGACCTGGGTCCTGGCAGGCTC 121
154 CCGTGTGAGCCCTGTGATTCACCTTAGTAGCTATGCTATGACACTGGGTCCTGGCAGGCTC 213

Db
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122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTATATCAATGATGGAAGTAATAATATCAAG 181
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274 CAGACTCCGTGAAGGCGCATTCACCACTCTCCAGAGACAAATTCGMAACACGCTGTATC 333

Dc		252	TCTTAAATGAGCCTGTAGAGCTTGAGACACA	CGCGCTGTATTACTGTGGAGAGAGACC	393
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Db 394 GAGGGGACTACTGGGGCCAGGAACTGTGTCACCGTCTCTCA 437

RESULT 9			
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LOCUS			PRI 01-JUN-2004
HSAS579107			

ACCESSION VERSION	variable region (IGHV-33 gene), clone T1.3.14.
AJ579107	
AJ579107.1	GI:47846392

SOURCE ORGANISM		
Homo sapiens (human)		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		

REFERENCE
AUTHORS
TITLE
JOURNAL
NUMBER
1
Dono, M.
Characterization of a novel CD5+ B cell population

REFERENCE	
AUTHORS	2 (bases 1 to 342)
TITLE	Dono, M.
JOURNAL	Direct Submission
Submitted	(07 MAY 2003) Dono M
	OncoTocia Medica C
	TestFuture

FEATURES	LOCATION/QUALIFIERS
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ITALY	
Nazionale	Ricecca sul Cancio, L. 90 R. Benzi 10, Genova, 16132,

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LOCUS       HSE5310
DEFINITION  H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION   Z14168.1
VERSION     Z14168.1 GI:30999
KEYWORDS    Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig
            variable region; immunoglobulin.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Cushtler A.M., Gauthier, L., Boubli, L., Fougereau, M. and
            Tonnelie, C.
TITLE       Mechanisms that generate human immunoglobulin diversity operate
            from the 8th week of gestation in fetal liver
JOURNAL     Eur. J. Immunol. 23 (1), 110-118 (1993)
MEDLINE    93122076
PUBMED     8419161
REFERENCE   2 (bases 1 to 398)
            Tonnelie, C.
            Direct Submission
            Submitted (09-JUN-1992) C. Tonnelie, Centre d'Immunologie
            Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE
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Qy	49 AGRTGCAAGCTGTGTGAGTCTGGGGAGGCCGTGTCACAGCTTGAGAGCTCT	108
Dd	62 CCTGTGCAGCTCTGTGATTCACCTTTGATATTATGCATCATGCACTGGGTCCGCAGGCTC	121
Qy	109 CCTGTGACGCTCTGTGATTCACCTTCAATACTTAGCATGCACTGGGTCCGCAGGCTC	168
Dd	122 CAGCCAAGGGCTGAGTGTGGTGCAGTTATATCATATGATGAAAGTAATAATCATATG	181
Qy	169 CAGCCAAGGGCTGAGTGTGGTGCAGTTATATCATATGATGAAAGTAATAATCATATG	228
Dd	182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAACAATTCOAAGAACCGCTGTATC	241
Qy	229 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAACAATTCOAAGAACCGCTGTATC	288
Dd	242 TGCAAAATGAACAGCTGTGAGCTGAGGACAGGGCTGTATTACTGTGCGAAAA-----	294
Qy	289 TGCAAATGAACAGCTGTGAGCTGAGGACAGGGCTGTATTACTGTGCGAAAAAGATCTCT	348
Dd	295 -----AAGGAAGCTACTGGGGCCAGGAAACCTGTATCACCGTCTCTCA	339
Qy	349 TCTACTACTTTGACTACTGGGGCCAGGAAACCTGTATCACCGTCTCTCA	398
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LOCUS	ABO67097	345 bp mRNA linear PRI 02-JUL-2002
DEFINITION	Homo sapiens IGH mRNA for immunoglobulin heavy chain VHJ region,	
LOCATION	partial cds, clone:aIm0184h.	
VERSION	ABO67097	
KEYWORDS	ABO67097.1 GI:21670250	
SOURCE	.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carartaria; Homniade; Homo. 1 Akahori,Y., Iba.Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ueki,Y., Honda,T., Katsumi,H., Okada,U., Miura,K. and Kurowsawa,Y. Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics Unpublished 2 (bases 1 to 345) Kurowsawa,Y.	JOURNAL REFERENCE AUTHORS

TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology, Kutsukake-cho, Toyake, Aichi 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
URL: <http://www.fujita-hu.ac.jp/immunology/>.

FEATURES
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QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGGCTGTATTAATCTGTGCG-----AAA 294
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RESULT 12
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DEFINITION Homo sapiens partial mRNA for Igm immunoglobulin heavy chain
ACCESSION HSA579114
VERSION AJ579114.1 GI:47846406
KEYWORDS IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Dono, M.
TITLE Characterization of a novel CDS+ B cell population

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 336)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2003) Dono M., Oncologia Medica C., Istituto Nazionale Ricerca sul Cancro, L. go R. Benzi 10, Genova, 16132, ITALY

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RESULT 13
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DEFINITION Homo sapiens partial mRNA for immunoglobulin gamma heavy chain variable region (IGHV3-30), clone M2-45 (m2h45), Kawasaki disease patient.
ACCESSION HSA300793
VERSION AJ300793.1 GI:12733989
KEYWORDS IGHV3-30 gene; immunoglobulin gamma heavy chain; Kawasaki disease; variable region.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 354)
 Leucht, S., Utenteuthen-Fischer, M.W., Gaeckle, G. and Fischer, P. The B cell superantigen-like interaction of intravenous immunoglobulin (IVIg) with Fab fragments of V(H) 3-23 and 3-30/3-30.5 germline gene origin cloned from a patient with Kawasaki disease is enhanced after IVIG therapy
 JOURNAL Clin. Immunol. 99 (1), 18-29 (2001)

MEDLINE 21185274
 PUBMED 11286538
 REFERENCE 2 (bases 1 to 354)
 Fischer, P.
 TITLE Direct Submission
 JOURNAL Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital, Molecular Biology Laboratory, Humboldt-University, Ziegelerstr. 5-9, Berlin, 10117, GERMANY

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 DEFINITION Sequence 2 from Patent WO0185797.
 ACCESSION AX300024
 VERSION AX300024.1 GI:17381484
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Rodriguez, M., Miller, D.J. and Pease, L.R. Human igm antibodies with the capability of inducing remyelination, and diagnostic and therapeutic uses thereof particularly in the central nervous system
 Patent: WO 0185797-A 2 15-NOV-2001;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)

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RESULT 15
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 DEFINITION Homo sapiens clone dns immunoglobulin heavy chain variable region mRNA, partial cds.
 ACCESSION AF115111
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 376)
 Smithson, S.L., Sivasubava, N., Huchins, W.A. and Westerink, M.A. Molecular analysis of the heavy chain of antibodies that recognize the capsular polysaccharide of *Neisseria meningitidis* in hu-PBMC reconstituted SCID mice and in the immunized human donor

JOURNAL Mol. Immunol. 36 (2), 113-124 (1999)
 MEDLINE 99305028
 PUBMED 10378683
 REFERENCE 2 (bases 1 to 376)
 AUTHORS Smithson, S.L., Srivastava, N., Hutchins, W.A. and Westerink, M.A.J.
 TITLE Direct Submision
 JOURNAL Submitted (17-DEC-1998) Medicine, Medical College of Ohio, 3000
 Arlington Ave, Toledo, OH 43614, USA

FEATURES

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CDS

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Query Match

Best Local Similarity 83.8%; Score 284; DB 9; Length 376;
 Matches 318; Conservative 0; Mismatches 20; Indels 12; Gaps 1;

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 Job time : 1725.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 17:46:48 ; Search time 356.464 Seconds
(without alignments)
5629.725 Million cell updates/sec

Title: US-09-403-107-145_COPY_1_339

Perfect score: 339
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1908:*
3: geneseqn2008:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
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8: geneseqn2003a:*
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10: geneseqn2003c:*
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12: geneseqn2004a:*
13: geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	372	2	AAV68538
2	301.2	88.8	729	12	ADN07003
3	294.8	87.0	396	10	ADG61027
4	289.2	85.3	342	12	ADG75774
5	284.4	83.9	357	12	ADJ26655
6	284	83.8	351	12	ADJ22042
7	284	83.8	351	12	ADJ22043
8	283.8	83.7	405	10	ADC61031
9	282.4	83.3	351	12	ADJ22044
10	282.4	83.3	351	12	ADJ22041
11	282	83.2	345	12	ADJ22052
12	281	82.9	354	6	ABK88453
13	280.8	82.8	351	12	ADJ22046
14	280.8	82.8	351	12	ADJ22045
15	280.6	82.8	349	13	ADG84379
16	280.6	82.8	349	13	ADG84379
17	280.6	82.8	404	10	ADG61047
18	280.6	82.8	404	10	ADG61043
19	279.2	82.4	351	12	ADJ22047
20	279	82.3	405	10	ADC61039

21	278.4	82.1	381	2	AAJ77236	AAJ77236 Human DA.
22	278.4	82.1	414	2	AAV68537	AAV68537 Nucleotid
23	278.4	82.1	1630	3	AAZ50588	AAZ50588 HD708CPV-
24	278.4	82.1	1630	3	AAZ50587	AAZ50587 HD708CPV-
25	277.4	81.8	405	10	ADC61035	ADC61035 Human ant
26	277.2	81.8	339	4	AAJ03438	AAJ03438 DNA encod
27	277.2	81.8	345	12	ADJ22049	ADJ22049 Anti-plat
28	277.2	81.8	2302	13	ACN41350	ACN41350 Human dia
29	276.6	81.6	369	2	AAJ60380	AAJ60380 Anti-TGF
30	276.2	81.5	400	6	ABJ38517	ABJ38517 Human col
31	275.8	81.4	405	10	ADC61051	ADC61051 Human ant
32	275.8	81.4	405	10	ADC61111	ADC61111 Human ant
33	275.6	81.3	339	4	AAJ03437	AAJ03437 DNA encod
34	275	81.1	345	2	AAJ60369	AAJ60369 Anti-TGF
35	275	81.1	350	2	AAJ60370	AAJ60370 Anti-TGF
36	274.6	81.0	354	6	ABA94330	ABA94330 MAb 6-2 h
37	274.6	81.0	366	12	ADP22127	ADP22127 Human ant
38	274.4	80.9	351	6	ABK88457	ABK88457 Human ant
39	274.4	80.9	376	10	ADB28450	ADB28450 Human ant
40	274.4	80.9	675	4	AAH41661	AAH41661 Human int
41	274.4	80.9	675	4	AAH30007	AAH30007 Anti-IL8
42	274.2	80.9	349	13	ADG84391	ADG84391 Human ant
43	274.2	80.9	349	13	ADG84391	ADG84391 Anti-EPO-
44	274.2	80.9	405	10	ADC61055	ADC61055 Human ant
45	274.2	80.9	405	10	ADC61067	ADC61067 Human ant

ALIGNMENTS

RESULT 1	AAV68538	standard; DNA; 372 BP.
ID	AAV68538	
AC	AAV68538	
XX		
DT	16-FEB-1999	(first entry)
DE	Nucleotide sequence of human D7.2 heavy chain variable region.	
XX		
KW	Human; D7.2 heavy chain variable region; receptor; antigen; tumour;	
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;	
XX	endocrine disease; degenerative disease; ss.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..372
FT		/*tag= a
FT		/product= "human D7.2 heavy chain variable region"
PN	WO9846645-A2.	
XX		
PD	22-OCT-1998.	
XX		
PF	14-APR-1998;	98WO-BP002180.
XX		
PR	14-APR-1997;	97EP-00106109.
XX		
PA	(KUF6/) KUFER P.	
PA	(RAUM/) RAUM T.	
XX		
PI	Kuifer P.	Raum T;
XX		
DR	WPI; 1998-594564/50.	
XX	P-PSDB; AAW80816.	
PT	Production of anti-human antigen receptors - by selecting a combination	
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from	
XX	a recombinant vector.	
XX		
PS	Claim 9; Fig 8; 84pp; English.	
XX		

CC This is the nucleotide sequence of the human D7.2 heavy chain variable
CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumors or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process
XX
SQ Sequence 372 BP, 86 A, 95 C, 110 G, 81 T, 0 U, 0 Other;

Query Match 100.0%; Score 339; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.6e-91;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGACACTGCTGAGTCTGGGGAGTCGTGTACACCTGGGGGCTCCTGAGACTC 60
DB 1 GAGGTGACACTGCTGAGTCTGGGGAGTCGTGTACACCTGGGGGCTCCTGAGACTC 60
QY 61 TCCGTGACGCTCTGATTCACCTTGTATGATTATGATGATGATGATGATGATGATGAT 120
DB 61 TCCGTGACGCTCTGATTCACCTTGTATGATTATGATGATGATGATGATGATGATGAT 120
QY 121 CCAAGGCAAGGGCTGGAGTGGGTGGCAATTATGATGATGATGATGATGATGATGATGAT 180
DB 121 CCAAGGCAAGGGCTGGAGTGGGTGGCAATTATGATGATGATGATGATGATGATGATGAT 180
QY 181 GAGAGTCCGTGAGAGGCGGATTCACATCTCCAGAGCAATTCAGAGACGCTGTAT 240
DB 181 GAGAGTCCGTGAGAGGCGGATTCACATCTCCAGAGCAATTCAGAGACGCTGTAT 240
QY 241 CTGCAATGAAACGCTGAGAGTGAAGACAGGCGTGTATTAATCTGTGCGAAAAAGAA 300
DB 241 CTGCAATGAAACGCTGAGAGTGAAGACAGGCGTGTATTAATCTGTGCGAAAAAGAA 300
QY 301 GGCTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 339
DB 301 GGCTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 339

RESULT 2

ADN07003
ID ADN07003 standard; DNA; 729 BP.
XX
AC ADN07003;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human BFGF bs-scFv antibody associated DNA.
XX
KW Bispecific single chain; bs-scFv; cancer;
XX epidermal growth factor receptor; EGFR; therapy; antibody; human; ds.
OS Homo sapiens.
XX
PN US2004071696-A1.
XX
PD 15-APR-2004.
XX
PF 04-APR-2003; 2003US-00406830.
XX
PR 05-APR-2002; 2002US-0370276P.
XX
PA (REGC) UNIV CALIFORNIA.
XX (FOXC-) FOX CHASE CANCER CENT.
XX
PI Adams GP, Horak EM, Weiner LM, Marks JD;
XX
DR WPI; 2004-328525/30.
XX
PT Novel bispecific antibody comprising first and second antibody joined to
XX each other and having binding specificity to different epitopes of
XX Epidermal Growth Factor Receptor protein, useful for treating cancer.
PT

XX
PS Claim 14; SEQ ID NO 20; 57pp; English.

CC The present invention provides bispecific single chain (bs-scFv) antibody
CC molecules which may be used to treat various forms of cancer associated
CC with the overexpression of the epidermal growth factor receptor (EGFR)
CC family. The invention is useful for specifically delivering an effector
CC molecule to a cell bearing a receptor from EGFR protein family chosen
CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
CC treatment of cancer. The present sequence is human BFGF bs-scFv antibody
CC associated DNA used in the invention.
XX
SQ Sequence 729 BP, 155 A, 196 C, 216 G, 162 T, 0 U, 0 Other;

Query Match 88.8%; Score 301.2; DB 12; Length 729;
Best Local Similarity 93.2%; Pred. No. 1.4e-79;
Matches 315; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 AGGTGACACTGCTGAGTCTGGGGAGTCGTGTACACCTGGGGGCTCCTGAGACTCT 61
DB 8 AGGTGACACTGCTGAGTCTGGGGAGTCGTGTACACCTGGGGGCTCCTGAGACTCT 67
QY 62 CCGTGTGACGCTCTGATTCACCTTGTATGATTATGATGATGATGATGATGATGATGAT 121
DB 62 CCGTGTGACGCTCTGATTCACCTTGTATGATTATGATGATGATGATGATGATGATGAT 127
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATGATGATGATGATGATGATGATGATGAT 181
DB 128 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATGATGATGATGATGATGATGATGATGAT 187
QY 182 CAGACTCCGTGAGAGGCGGATTCACATCTCCAGAGCAATTCAGAGACGCTGTATC 241
DB 188 CAGACTCCGTGAGAGGCGGATTCACATCTCCAGAGCAATTCAGAGACGCTGTATC 247
QY 242 TGCATATGAAACGCTGAGAGTGAAGACAGGCGTGTATTAATCTGTGCGAAAAAGAA 301
DB 248 TGCATATGAAACGCTGAGAGTGAAGACAGGCGTGTATTAATCTGTGCGAAAAAGAA 307
QY 302 GCTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 339
DB 308 TAACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 345

RESULT 3

AD6C1027
ID AD6C1027 standard; DNA; 396 BP.
XX
AC AD6C1027;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human anti-CD45RB monoclonal antibody DNA, SEQ ID NO 54.
XX
KW monoclonal antibody; CD45RB; antigen; cell proliferation;
XX immunosuppressive; neuroprotective; tissue rejection; organ rejection;
XX autoimmune disease; multiple sclerosis; human; anti-CD45RB; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003048327-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038540.
XX
PR 03-DEC-2001; 2001US-0337276P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Foltz I, Babcock J, Palachumpat V, Yang X, King CT;
XX
DR WPI; 2003-558954/52.
XX
PT P-PSDB; AD6C1028.
DR

XX New anti-CD45RB monoclonal antibody, useful for treating an autoimmune
PT disease e.g. multiple sclerosis.
XX disclosure; SEQ ID NO 54; 121pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy chain having a sequence chosen from one of 22 fully defined
CC sequences comprising 135-147 amino acids, given in the specification, and
CC is specific for CD45RB antigen. The invention further relates to:
CC inhibiting cell proliferation associated with the expression of CD45RB
CC antigen; and treating a disease associated with the expression of a
CC CD45RB antigen in a patient. The monoclonal antibody has the activities
CC of immunosuppressive and neuroprotective. The monoclonal antibody is
CC useful for treating the rejection of a mammalian cell, tissue or organ,
CC especially an autoimmune disease in a mammal, especially a human e.g.
CC multiple sclerosis. This polynucleotide sequence represents a DNA
CC encoding a human protein of the anti-CD45RB monoclonal antibody of the
CC invention.
XX
XX Sequence 396 BP; 84 A; 92 C; 124 G; 96 T; 0 U; 0 Other;
SO
Query Match 87.0%; Score 294.8; DB 10; Length 396;
Best Local Similarity 92.0%; Pred. No. 9e-78;
Matches 311; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTCT 61
DB 59 AGGTGACGCTGCTGAGTCTGGGGGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTCT 118
QY 62 CCTGTGACGCTGCTGAGTCTGGGGGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTCT 121
DB 119 CCTGTGACGCTGCTGAGTCTGGGGGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTCT 178
QY 122 CAGGCAAGGCGGCTGAGTGGTGGGAGTATATCATATGATGAGAGTAATAATATCTATG 181
DB 179 CAGGCAAGGCGGCTGAGTGGTGGGAGTATATCATATGATGAGAGTAATAATATCTATG 238
QY 182 CAGACTCCGCTGAGGCGGCTGAGTGGTGGGAGTATATCATATGATGAGAGTAATAATATCTATG 241
DB 239 CAGGCTCCGCTGAGGCGGCTGAGTGGTGGGAGTATATCATATGATGAGAGTAATAATATCTATG 298
QY 242 TGCATATGAAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGGGAAAAAGAGG 301
DB 299 TGCATATGAAACAGCTGAGAGTGAAGACACGGCTGTGATTACTGTGGGAAAAAGAGG 358
QY 302 GCTACTGGGGCCAGGAGACCTGTGTCACCGTCTCTCA 339
DB 359 ACTACTGGGGCCAGGAGACCATGTCACTCTCTCTCA 396
RESULT 4
ADQ75774
ID ADQ75774 standard; cDNA; 342 BP.
XX
XX ADQ75774;
XX
XX 07-OCT-2004 (first entry)
XX
XX Anti-IL-8 antibody, VH 3-33, VH coding sequence.
XX
XX antibody; heavy chain, light chain, variable region; constant region; VH;
XX VL; monoclonal antibody; Mab; Interleukin-8; IL-8;
XX complementarity determining region; CDR; inflammation;
XX hyperproliferation; skin disorder; PPP; psoriasis; plaque psoriasis;
XX gutate type psoriasis; bullous skin disease; bullous pemphigoid;
XX contact dermatitis; eczema; erythematous; atopic dermatitis;
XX immune disorder; autoimmune disorder; inflammatory disease;
XX psoriatic arthritis; systemic scleroderma; sclerosis;
XX inflammatory bowel disease; IBD; Crohn's disease; ulcerative colitis;
XX acute lung injury; acute respiratory distress syndrome;
XX adult respiratory distress syndrome; meningitis; encephalitis; uveitis;
XX multiple myeloma; glomerulonephritis; nephritis; asthma; atherosclerosis;

KW leukocyte adhesion deficiency; multiple sclerosis; Raynaud's syndrome;
KW Sjogren's syndrome; juvenile onset diabetes; Reiter's disease;
KW Behcet's disease; immune complex nephritis; Iga nephropathy;
KW IgM polyneuropathy; immune-mediated thrombocytopenia;
KW acute idiopathic thrombocytopenic purpura; haemolytic anaemia;
KW chronic idiopathic thrombocytopenic purpura; lupus erythematosus;
KW myasthenia gravis; lupus nephritis; lupus erythematosus;
KW rheumatoid arthritis; ankylosing spondylitis; pemphigus; Graves' disease;
KW Hashimoto's thyroiditis; Wegener's granulomatosis; Omen's syndrome;
KW chronic renal failure; autoimmune thyroid disease;
KW acute infectious mononucleosis; HIV; herpes virus associated disease;
KW common cold; human rhinovirus; coronavirus; enterovirus; herpes virus;
KW influenza virus; parainfluenza virus; respiratory syncytial virus;
KW adenovirus infection; bacteria pneumonia; sepsis; cerebral stroke;
KW cerebral edema; ischemia-reperfusion injury; hepatitis C; thrombolysis;
KW cardiopulmonary bypass; percutaneous coronary intervention; PCI;
KW coronary artery bypass; cardiac transplantation;
KW isolated cerebral infarction; myocarditis; pericarditis;
KW acute myocardial infarction; myocarditis; pericarditis;
KW Lieberman-Sachs endocarditis; chronic obstructive pulmonary disease; COPD;
KW alveolitis; obliterating bronchiolitis; cystic fibrosis;
KW allergic aspergillosis; Loeffler's syndrome; sclerosing cholangiolitis;
KW chronic cystitis; tubulo-interstitial nephritis;
KW severe acute respiratory syndrome; SARS; large vessel vasculitis;
KW giant cell arteritis; polymyalgia rheumatica; Takayasu arteritis;
KW medium-sized vessel vasculitis; polyarteritis nodosa;
KW localized polyarteritis nodosa; Kawasaki disease;
KW small vessel vasculitis; Churg-Straus syndrome;
KW microscopic polyarteritis; cryoglobulinemic vasculitis;
KW leucocytoclastic angitis; secondary vasculitis; rheumatoid vasculitis;
KW systemic lupus erythematosus; isolated sacroiliitis; SAPHO syndrome;
KW discitis; postoperative discitis; subacute thyroiditis;
KW cicatricial pemphigoid; dermatitis herpetiformis;
KW subacute pustular dermatosis; epidermolysis bullosa acquisita; rosacea;
KW acute febrile dermatosis; granuloma annulare; Sweet's syndrome;
KW pyoderma gangrenosum; acne; acne conglobata; sarcoidosis;
KW relapsing polycondritis; familial Mediterranean fever; panniculitis;
KW erythema nodosum; Weber-Christian's disease; retroperitoneal fibrosis;
KW osteoporosis; osteolytic metastases; gastric cancer; colorectal cancer;
KW urtic bladder cancer; tumour growth; melanoma; thyroid carcinoma;
KW transitional cell carcinoma; trichilemmoma; squamous cell carcinoma;
KW breast cancer; ss; gene.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..342
XX FT /*tag= a
XX FT /product= "VH 3-33 "
XX
XX WO2004058797-A2.
XX
XX 15-JUL-2004.
XX
XX 16-DEC-2003; 2003MO-US040039.
XX
XX 16-DEC-2002; 2002US-043728P.
XX
XX (MEDA-) MEDAREX INC.
XX (GENM-) GENMAB AS.
XX
XX Teeling J, Parren P, Baadsgaard ODMS, Hudson D, Petersen J;
XX WPI; 2004-534122/51.
XX P-PsDB; ADQ75776.
XX
XX New isolated human monoclonal antibodies binding to human IL-8 having a
PT heavy and/or light chain encoded by a nucleic acid, useful for preventing
PT or treating cancer, immune disorders, inflammatory diseases and
PS angiogenic conditions.
XX
XX Claim 22; SEQ ID NO 9; 102pp; English.
XX

cells in CNS axons in a mammal (comprising administering a monoclonal antibody, or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CNS), treating or preventing a demyelinating disease of the CNS in a mammal (comprising administering a monoclonal antibody, or mixtures, monomers, active fragments; or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CNS, and to stimulate remyelination of axons of the CNS), stimulating, in vitro, the proliferation of glial cells from mixed cell culture, stimulating remyelination of CNS axons in a mammal, a DNA sequence (or degenerate variant of it) which encodes an antibody (or a peptide analogue, hapten, or active fragment of it, where the DNA sequence consists of a sequence encoding an anti-IGM antibody), a probe capable of screening for the antibody, an assay for screening drugs and other agents for the ability to modulate the production or mimic the activities of mAb SH1M22, SH1M46, or combinations of them, a recombinant virus transformed with recombinant antibody nucleic acid or vector, imaging a portion of the CNS using the antibody and diagnosing or monitoring demyelination and/or remyelination of the CNS comprising using CNS image. The antibody is used to stimulate remyelination of CNS axons, and to stimulate the proliferation of glial cells in CNS axons, optionally in vitro. The antibody is used to treat or prevent a demyelinating disease of the CNS in a human or domestic animal, such as multiple sclerosis, or a disease, other injury or dysfunction of the CNS, preferably the mammal is a mouse infected with Strain DA of Theiler's murine encephalomyelitis virus. The antibody is used to treat a spinal cord injury and used to screen drugs and other agents for the ability to modulate the production or mimic the activities of the antibody. The antibody can be used to image a portion of the CNS which can be used to diagnose or monitor demyelination and/or remyelination of the CNS. The present sequence is a cDNA for a variable region of a human anti-IGM antibody.

Sequence 357 BP; 81 A; 89 C; 107 G; 80 T; 0 U; 0 Other;

Query Match 83.9%; Score 284.4; DB 12; Length 357;
Best Local Similarity 90.4%; Pred. No. 1.1e-74;
Matches 322; Conservative 0; Mismatches 16; Indels 18; Gaps 1;

```
QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGTCTGTATACCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGAGTCTGGGGGAGTCTGTATACCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCGTGTACAGCTCTGATTCACCTTGTATGATTAATGATGACCTGGGCTCCGACAGCTC 121
DB 62 CCGTGTACAGCTCTGATTCACCTTGTATGATTAATGATGACCTGGGCTCCGACAGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGTAATTAATTAATCTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGTAATTAATTAATCTATG 181
QY 182 CAGACTCCGTAAGGGCCGATTCACCATCTCCAGAACATTCACAGAACACCGCTGTATC 241
DB 182 CAGACTCCGTAAGGGCCGATTCACCATCTCCAGAACATTCACAGAACACCGCTGTATC 241
QY 242 TGCATATGACACCTTGAAGCTGAGACACGGCTGTATTAATCTGTGGAAAGAGCTGA 301
DB 242 TGCATATGACACCTTGAAGCTGAGACACGGCTGTATTAATCTGTGGAAAGAGCTGA 301
QY 299 -----AAGCTTACTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 339
DB 302 CTGCTATTCCTTACTTGTACTATGAGGGGCGAGGAAACCTGTGACCGTCTCTCTCA 357
```

RESULT 6
AD122042
ID AD122042 standard; DNA; 351 BP.

AC AD122042;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-platelet autoantibody related heavy chain nucleotide H37 SEQ:5.

XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition; platelet aggregation inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
XX thrombolytic; human; gene; de.
OS
OS Homo sapiens.
XX Synthetic.
PN WO2004005890-A2.
XX
XX 15-JAN-2004.
XX
XX 03-JUL-2003; 2003WO-US021304.
XX
XX 03-JUL-2002; 2002US-0394352P.
XX
XX 18-SEP-2002; 2002US-0411694P.
XX
XX (UYPF-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
PI
XX WPI; 2004-142998/14.
DR P-PSDB; AD122095.
XX
PS Claim 21; SEQ ID NO 5; 232bp; English.

CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (1) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (1) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (1) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

Sequence 351 BP; 79 A; 87 C; 108 G; 77 T; 0 U; 0 Other;

Query Match 83.8%; Score 284; DB 12; Length 351;
Best Local Similarity 90.9%; Pred. No. 1.5e-74;
Matches 318; Conservative 0; Mismatches 20; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGGGAGTCTGTATACCTGGGGGCTCCCTGAGACTCT 61

DB 2 AGGTGACGCTGGTGGAGTCTGGGGGAGCGGTGGTCCAGCTGGAGGTCCTGAGACTCT 61
QY 62 CCTGGACACCTCTGGATTCACCTTTGATGATTAAGTCCATGACCTGGGTCGCCGACGGCTC 121
DB 62 CCGTGACACCTCTGGATTCACCTTTGATGATTAAGTCCATGACCTGGGTCGCCGACGGCTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATATCATATGATGAGTAATAAATACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATATCATATGATGAGTAATAAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCCATTCACATCTCCAGAGACAATTCGAAGAACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCCATTCACATCTCCAGAGACAATTCGAAGAACGCTGTATC 241
QY 242 TGCATAATGAACAGCCTGAGACCTGAGACACCGCTGTGTATTAATCTGTGCAAGAGTGGGG 298
DB 242 TGCATAATGAACAGCCTGAGACCTGAGACACCGCTGTGTATTAATCTGTGCAAGAGTGGGG 301
QY 299 -----AAGGCTACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 339
DB 302 TAGCAGCTTTTGACTACTGTGGGGCAGGGAACCTGGTCAACCGTCTCTCA 351

RESULT 7
AD122043
ID AD122043 standard; DNA; 351 BP.

AC AD122043;
XX
DT 22-APR-2004 (first entry)

XX Anti-platelet autoantibody related heavy chain nucleotide H38 SEQ:6.

KM anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KM thrombus; platelet adhesion inhibitor;
KM thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KM idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
XX thrombolytic; human; gene; ds.

OS Homo sapiens.
XX Synthetic.

PN W02004005890-A2.

XX 15-JAN-2004.

PF 03-JUL-2003; 2003WO-US021304.

XX 03-JUL-2002; 2002US-0394352P.

PR 18-SEP-2002; 2002US-0411694P.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2004-142998/14.

XX P-PSDB; AD122096.

PS Claim 21; SEQ ID NO 6; 232BP; English.

XX The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component;

CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (1) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (1) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

XX Sequence 351 BP; 79 A; 86 C; 109 G; 77 T; 0 U; 0 Other;

XX Query Match 83.8%; Score 284; DB 12; Length 351;
XX Best Local Similarity 90.9%; Pred. No. 1,5e-74;
XX Matches 318; Conservative 0; Mismatches 20; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGGTGGAGTCTGGGGGAGCGGTGGTCCAGCTGGAGACTCT 61

DB 2 AGGTGACGCTGGTGGAGTCTGGGGGAGCGGTGGTCCAGCTGGAGACTCT 61

QY 62 CCTGTGACACCTCTGGATTCACCTTTGATGATTAAGTCCATGACCTGGGTCGCCGACGGCTC 121

DB 62 CCTGTGACACCTCTGGATTCACCTTTGATGATTAAGTCCATGACCTGGGTCGCCGACGGCTC 121

QY 122 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATATCATATGATGAGTAATAAATACTATG 181

DB 122 CAGGCAAGGGGCTGGAGTGGTGGCAGTTATATCATATGATGAGTAATAAATACTATG 181

QY 182 CAGACTCCGTGAAGGGCCCATTCACATCTCCAGAGACAATTCGAAGAACGCTGTATC 241

DB 182 CAGACTCCGTGAAGGGCCCATTCACATCTCCAGAGACAATTCGAAGAACGCTGTATC 241

QY 242 TGCATAATGAACAGCCTGAGACCTGAGACACCGCTGTGTATTAATCTGTGCAAGAGTGGGG 298

DB 242 TGCATAATGAACAGCCTGAGACCTGAGACACCGCTGTGTATTAATCTGTGCAAGAGTGGGG 301

QY 299 -----AAGGCTACTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 339

DB 302 TAGCAGCTTTTGACTACTGTGGGGCAGGGAACCTGGTCAACCGTCTCTCA 351

RESULT 8

AD61031
ID AD61031 standard; DNA; 405 BP.

AC AD61031;
XX
DT 18-DEC-2003 (first entry)

XX Human anti-CD45RB monoclonal antibody DNA, SEQ ID NO 58.

DE Human anti-CD45RB monoclonal antibody; antigen; cell proliferation;

XX monoclonal antibody; CD45RB; antigen; tissue rejection; organ rejection;

KW immunosuppressive; neuroprotective; tissue rejection; organ rejection;

XX autoimmune disease; multiple sclerosis; human; anti-CD45RB; gene; ds.

OS Homo sapiens.
XX

XX Homo sapiens.
 OS Synthetic.
 XX MO2004005890-A2.
 XX 15-JAN-2004.
 XX 03-JUL-2003; 2003WO-US021304.
 XX 03-JUL-2002; 2002US-0394352P.
 XX 18-SEP-2002; 2002US-0411694P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX MPI; 2004-142998/14.
 XX P-PSDB; AD122105.
 XX Claim 21; SEQ ID NO 15; 232bp; English.
 CC The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.

Sequence 345 BP; 81 A; 86 C; 99 G; 79 T; 0 U; 0 Other;

Query Match 83.2%; Score 282; DB 12; Length 345;
 Best Local Similarity 91.0%; Pred. No. 5.7e-74;
 Matches 313; Conservative 0; Mismatches 25; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGATGACCTGGGGGCTCTGAGACTCT 61
 DB 2 AGGTGAGCTGCTGAGTCTGGGGAGTCTGTGATGACCTGGGGGCTCTGAGACTCT 61
 QY 62 CCTGTGCAAGCTCTGTGATTCACCTTTGATGATATGATCCATGACCTGGGTCCGACGCTC 121
 DB 62 CCTGTGCAAGCTCTGTGATTCACCTTTGATGATATGATCCATGACCTGGGTCCGACGCTC 121

QY 122 CAGGCAAGGGGCTGGAGTGGGCTGAGTTATATCATATGATGGAATTAATACTANG 181
 DB 122 CAGGCAAGGGGCTGGAGTGGGCTGAGTTATATCATATGATGGAATTAATACTANG 181
 QY 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAGCTGTATC 241
 DB 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACAGCTGTATC 241
 QY 242 TGCATAATGAACAGCTGAGAGACACGGCTGTGTATTACTGTGCGAAAAAGAA- 300
 DB 242 TGCATAATGAACAGCTGAGAGACACGGCTGTGTATTACTGTGCGAAAAAGAA- 300
 QY 301 -----GGCTACTGGGGCCAGGGAACCTGCTGATCCGCTCCCA 339
 DB 302 CCTTGACTACCGGGCCAGGGAACCTGCTGATCCGCTCTTCA 345

RESULT 12
 ABR88453
 ID ABR88453 standard; cDNA; 354 BP.
 AC ABR88453;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human anti-CD40 monoclonal antibody 9F7 VH.1 region cDNA.
 XX
 KW Human; VH.1; heavy chain variable region; CD40; ss; gene;
 KW autoimmune disease; systemic lupus erythematosus; psoriasis;
 KW multiple sclerosis; inflammatory bowel disease; Crohn's disease;
 KW rheumatoid arthritis; organ rejection; lymphoma; non-Hodgkin's lymphoma;
 KW monoclonal antibody; B cell; glycoprotein; proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..354
 FT /tag= a
 FT /product= "9F7 heavy chain variable region"
 FT /partial
 FT /note= "No start or stop codon shown"
 XX
 PN MO200228904-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US030857.
 XX
 PR 02-OCT-2000; 2000US-0237556P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chu K, Wang C, Yoshihara C, Donnelly JJ;
 DR MPI; 2002-405169/43.
 DR P-PSDB; ABG30463.
 XX
 PT A human anti-CD40 monoclonal antibody or fragment useful for inhibiting proliferation, growth or differentiation of a normal human B cells and treating autoimmune disease such as rheumatoid arthritis or systemic lupus erythematosus.
 PT
 PS Claim 11; Fig 11; 75bp; English.
 XX
 CC The invention relates to a human monoclonal antibody or fragment capable of specifically binding to a human CD40 antigen (a glycoprotein expressed on the surface of human B cells), where the antibody or fragment is free of significant agonistic activity, when it binds to the CD40 antigen, and the growth or differentiation is inhibited. The fragments comprise the complementarily determining region (CDR) of the light and heavy chains of the monoclonal antibodies secreted by a hybridoma consisting of 15B8, 20C4, 12D9, 9F7 and 13F4. Also included are the nucleic acids encoding

RESULT 14
AD122045
ID AD122045 standard; DNA; 351 BP.
XX
XX AC
XX AD122045;
DT 22-APR-2004 (first entry)
XX
XX Anti-platelet autoantibody related heavy chain nucleotide H40 SEQ:8.
XX
XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human; gene; ds.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004005890-A2.
XX
XX 15-JAN-2004.
XX
XX 03-JUL-2003; 2003WO-US021304.
XX
XX 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX WPI; 2004-142998/14.
DR P-PSDB; AD122098.
XX
XX Claim 21; SEQ ID NO 8; 232bp; English.

The present invention describes a method (M1) for identifying an anti-platelet autoantibody (1) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (1) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (1) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the

CC	present	Invention.
XX	Sequence 351 BP; 79 A; 88 C; 107 G; 77 T; 0 U; 0 Other;	
XX	Query Match	82.8%; Score 280.8; DB 12; Length 351;
XX	Best Local Similarity	90.3%; Pred. No. 1.3e-73;
XX	Matches 316; Conservative	0; Mismatches 22; Indels 12; Gaps 1
QY	2 AGGTGACGCTGCTGAGTCTTGGGGAGTCTGTGTACACGCTTGGGGGTTCCCTGAGACTCT	61
DB	2 AGGTGACGCTGCTGAGTCTTGGGGAGGCGTGTCTCAGCTGGAGGTCCTGAGACTCT	61
QY	62 CCTGTGACGCTCTTGAGATTACCTTTGATGATTAATGATCCATGACACTGGGTCCGACGCTC	121
DB	62 CCTGTGACGCTCTTCAATTCACCTTCAAGTAATAATGATCACTAGCACTGGGTCCGACGCTC	121
QY	122 CAGGCAAGGGGCTGAGATGGGTGGCAGTTATATCATATGATGGAAGTAAATAACTATG	181
DB	122 CAGGCAAGGGGCTGAGATGGGTGGCAGTTATATCATATGATGGAAGTAAATAACTATG	181
QY	182 CAGACTCCGTGAAAGGGCGGATTTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC	241
DB	182 CAGACTCCGTGAAAGGGCGGATTTCACATCTCCAGAGCAATTCGAAGAACGCTGTATC	241
QY	242 TGCAAATGAACAGCCTGAGACTGAGACACAGCGCTGTATTAATCTGTGCGAAAAAGC---	298
DB	242 TGCAAATGAACAGCCTGAGACTGAGACACAGCGCTGTATTAATCTGTGCGAAAAAGC---	298
QY	299 -----AAGGCTACTGGGGCCAGGGAACCTGTGTACCGTCCCTCA	339
DB	302 TAGCGGCTTTTGACTACTGCGGGCCAGGGAACCTGTGTACCGTCCCTCA	351
RESULT 15		
ID	ADS84379	standard; DNA; 349 BP.
XX	ADS84379;	
AC	18-NOV-2004	(first entry)
DT		
XX		
DE	Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:18.	
XX	human; erythropoietin receptor; EPO receptor;	
KW	erythropoietin receptor binding antibody; EPO receptor binding antibody;	
KW	antianemic; neuroprotective; vulnerrary; gene therapy; aplasia; anaemia;	
KW	wound healing; neural cell damage protection;	
KW	neural tissue damage protection; brain injury; spinal cord injury;	
KW	stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;	
KW	ds.	
XX		
OS	Homo sapiens.	
XX		
XX	WO2004035603-A2.	
XX		
PD	29-APR-2004.	
XX		
PF	14-OCT-2003; 2003WO-US032243.	
XX		
PR	14-OCT-2002; 2002US-00269711.	
PR	10-OCT-2003; 2003US-00684109.	
XX		
PA	(ABBO) ABBOTT LAB.	
PI	Devries PJ, Green JL, Ostrow DH, Reilly EB, Wieler J;	
XX		
XX	WPI; 2004-348433/32.	
DR	P-PSDB; ADS84380.	
XX		
PT	New antibodies that bind to or activate an endogenous human	
PT	erythropoietin receptor, useful for diagnosing, preventing or treating	
PT	disorders associated with dysfunctional erythropoietin receptor, e.g.	
PT	anemia.	

XX Claim 47; SEQ ID NO 18; 192pp; English.

PS The present invention describes an antibody or its fragment that binds to
CC or activates an endogenous activity of a human erythropoietin (EPO)
CC receptor in a mammal, but does not interact with a peptide having a
CC sequence of 30 amino acids (SEQ ID NO:1, AD84362). Also described: (1)
CC methods of modulating or activating an endogenous activity of a human EPO
CC receptor in a mammal, comprising administering to the mammal a
CC therapeutic amount of the above antibody or its fragment to modulate or
CC activate the receptor; (2) a method of treating a mammal suffering from
CC aplasia, comprising administering to the mammal a therapeutic amount of
CC the above antibody or its fragment to modulate or activate the receptor;
CC (3) a pharmaceutical composition comprising a therapeutic amount of the
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
CC an isolated and purified polynucleotide sequence, and their fragments,
CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antianaemic, neuroprotective and vulnary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence encodes a human anti-EPO-R antibody heavy
CC chain variable region, which is given in the exemplification of the
CC present invention.

XX
SQ Sequence 349 BP; 78 A; 85 C; 110 G; 76 T; 0 U; 0 Other;

Query Match 82.8%; Score 280.6; DB 13; Length 349;
Best Local Similarity 90.5%; Pred. No. 1.5e-73;

Matches 314; Conservative 0; Mismatches 24; Indels 9; Gaps 1;

QY	2	AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGATCAGGCTGGGGGTCCTGAGACTCT	61
DB	2	AGGTGAGCTGGTGGTGGAGTGGGGGAGGGGTGGTCCAGCTGGAGACTCT	61
QY	62	CCTGTGCAGCTCTGTGATTCACTTTGATGATTATGCCATGCACTGGGTCGCCAGGCTC	121
DB	62	CCTGTGCAGCTGTGATTCACTTCAGTAAATATGCACTGGGTCGCCAGGCTC	121
QY	122	CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATAATACTATG	181
DB	122	CAGGCAAGGGGCTGAGTGGGTGGCAGTTTATGATGATGAGTAATAATACTATG	181
QY	182	CAGACTCCGTGAAGGGCCGATTCCACATCTCCAGAGCAATTCCAGAAACACGCTGTATC	241
DB	182	CAGACTCCGTGAAGGGCCGATTCCACATCTCCAGAGCAATTCCAGAAACACGCTGTATC	241
QY	242	TGCAATGTAACAGCTGAGAGCTGAGAGACAGGCTGTATTACTGTGCGA-----	292
DB	242	TGCAATGTAACAGCTGAGAGCTGAGAGACAGGCTGTATTACTGTGCGAGAGGTCGT	301
QY	293	AAAAGGAGGCTACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA	339
DB	302	ACTACTTTACTACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA	348

Search completed: September 11, 2005, 20:25:57
Job time : 360.464 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 18:08:48 ; Search time 2724.33 Seconds
(without alignments)
4736.504 Million cell updates/sec

Title: US-09-403-107-145_COPY_1_339

Perfect score: 339

Sequence: 1 gaggtgcagcgcgcgcagtc.....ccctgcgtaccgctccctca 339

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	EST:	Score	Query Match	Length	ID	Description
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2: gb-est2:*	2: 274.2	80.9	788	4	BG342203	BG342203 602462276
3: gb-est3:*	3: 274.2	80.9	870	4	BG759649	BG759649 602713342
4: gb-est4:*	4: 274.2	80.9	964	2	BF663281	BF663281 602144406
5: gb-est5:*	5: 274.2	80.9	991	4	BF974524	BF974524 602243430
6: gb-est6:*	6: 274.2	80.9	1010	2	BF663436	BF663436 602144593
7: gb-est7:*	7: 273.2	80.6	846	4	BG755572	BG755572 602716255
8: gb-est8:*	8: 272.6	80.4	912	4	BG756211	BG756211 602713521
9: gb-est9:*	9: 271.8	80.2	413	5	BX344075	BX344075 602713521
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	11: 269.6	79.5	899	5	BQ420418	BQ420418 AGENCOURT
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	14: 266.8	78.7	894	2	BQ708235	BQ708235 AGENCOURT
	15: 266.6	78.6	456	4	BG503730	BG503730 602549705
	16: 266.6	78.6	902	5	BX346850	BX346850 602549705
	17: 266.4	78.6	1228	5	BM920476	BM920476 AGENCOURT
	18: 266.2	78.5	761	4	BG757080	BG757080 602715111
	19: 265.8	78.4	413	5	BX399298	BX399298 602715111
	20: 264.8	78.1	918	5	BQ710537	BQ710537 AGENCOURT
	21: 264.6	78.1	621	6	CD687626	CD687626 EST147 h
	22: 263.6	77.8	436	6	AM402311	AM402311 UI-HF-BKO
	23: 263.2	77.6	750	4	BF976111	BF976111 602244955
	24: 262.4	77.4	430	5	BX480277	BX480277 DKF2p6860

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	261.8	77.2	950	5	BQ708952	BQ708952 AGENCOURT
26	261.4	77.1	536	2	AM402624	AM402624 UI-HF-BKO
27	260.8	76.9	907	5	BQ708724	BQ708724 AGENCOURT
28	260.8	76.9	1001	5	BM914366	BM914366 AGENCOURT
29	259.8	76.6	891	5	BUI50876	BUI50876 AGENCOURT
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31	259.2	76.5	930	4	BG755605	BG755605 602716292
32	258.6	76.3	802	4	BG755625	BG755625 602713557
33	257	75.8	999	5	BQ707443	BQ707443 AGENCOURT
34	255.2	75.3	415	5	BX456327	BX456327 602713527
35	254.6	75.1	511	2	AM402453	AM402453 UI-HF-BKO
36	253.8	74.9	937	5	BQ706852	BQ706852 AGENCOURT
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38	253	74.6	405	2	AM402449	AM402449 UI-HF-BKO
39	253	74.6	962	5	BQ706534	BQ706534 AGENCOURT
40	253	74.6	1000	5	BQ712690	BQ712690 AGENCOURT
41	251.6	74.2	891	5	BQ709554	BQ709554 AGENCOURT
42	251	74.0	889	5	BQ709105	BQ709105 AGENCOURT
43	251	74.0	925	5	BQ706858	BQ706858 AGENCOURT
44	251	74.0	986	5	BQ710656	BQ710656 AGENCOURT
45	250.4	73.9	648	4	BG340670	BG340670 602462250

ALIGNMENTS

RESULT 1	BG340648	678 bp	mrna	linear	EST 27-FEB-2001
LOCUS	602462226P1 NIH_MGC_48	Homo sapiens	cdna	clone	IMAGE:4574935 5',
DEFINITION	BG340648	1	GI:13147086		
ACCESSION	BG340648				
VERSION	BG340648.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 678)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: http://image.lnh.gov Plate: L1CM1285 row: d column: 08 High quality sequence stop: 666. Location/Qualifiers 1. 678 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4574935" /tissue_type="Primary B-cells from tonsils (cell line)" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_48" /note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."				
ORIGIN					

Query Match 80.9%; Score 274.2; DB 4; Length 678;
Best Local Similarity 95.6%; Pred. No. 1.2e-71;
Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 130 AGGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 189
OY 62 CCTGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 121
DB 190 CCTGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 249
OY 122 CAGGCAAGGGGCTGAGTGTGGTGGCAGTTATATATGATGAGTAAGTAATAATCTATG 181
DB 250 CAGGCAAGGGGCTGAGTGTGGTGGCAGTTATATATGATGAGTAAGTAATAATCTATG 309
OY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACACGCTGTATC 241
DB 310 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACACGCTGTATC 369
OY 242 TGCAATGAAACAGCTGAGAGCTGAGGACAGCGCTGTATTAATCTGTGCGAAAA 296
DB 370 TGCAATGAAACAGCTGAGAGCTGAGGACAGCGCTGTATTAATCTGTGCGAAAA 424

RESULT 2
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VERSION BG342203.1 GI:13148641
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 788)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LINC1287 row: m column: 20
High quality sequence stop: 687.

FEATURES

source

1..788
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4575931"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match

80.9%; Score 274.2; DB 4; Length 788;
Best Local Similarity 95.6%; Pred. No. 1.2e-71;

Best Local Similarity 95.6%; Pred. No. 1.2e-71;
Matches 282; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2 AGGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 61
DB 129 AGGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 188
OY 62 CCTGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 121
DB 189 CCTGTGACAGCTCTGAGTCTGGGGAGTGTGTGTAACAGCTGGGGGGTCCCTGAGACTCT 248
OY 122 CAGGCAAGGGGCTGAGTGTGGTGGCAGTTATATATGATGAGTAAGTAATAATCTATG 181
DB 249 CAGGCAAGGGGCTGAGTGTGGTGGCAGTTATATATGATGAGTAAGTAATAATCTATG 308
OY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACACGCTGTATC 241
DB 309 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCGAAGAACACGCTGTATC 368
OY 242 TGCAATGAAACAGCTGAGAGCTGAGGACAGCGCTGTATTAATCTGTGCGAAAA 296
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RESULT 3
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DEFINITION mRNA sequence.
ACCESSION BG759649
VERSION BG759649.1 GI:14070302
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LINC1699 row: d column: 11
High quality sequence stop: 764.

FEATURES

source

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4853338"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match

80.9%; Score 274.2; DB 4; Length 870;
Best Local Similarity 95.6%; Pred. No. 1.2e-71;

	Matches	282;	Conservative	0;	Mismatches	13;	Indels	0;	Gaps	0;
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Dd	130	AGTTGCACCTGGTAGTGCTGGGGGAGGGGTGCTCAGCTCGGGAGTCCCTGA	CACTT	189						
Qy	62	CCTGTGACAGCCTCTGATTCACCTTTGATTGATTATGATGCATGCACTGGTCCG	CGACGCTC	121						
Dd	190	CCTGTGACAGCCTCTGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCG	CAGGCTC	249						
Qy	122	CAGGCAAGGGGCTGGAGTGGGGGAGTTATTCATATGATGAAAGTAATAA	TCTGTG	181						
Dd	250	CAGGCAAGGGGCTGGAGTGGGGGAGTTATTCATATGATGAAAGTAATAA	TCTGTG	309						
Qy	182	CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACAATTCCAA	AACGCTGTATC	241						
Dd	310	CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACAATTCCAA	AACGCTGTATC	369						
Qy	242	TGCAAAATTAACGCTGAGAGCTGAGGACAAGGCTGTGATTAATCACTGTG	AAAAA	256						
Dd	370	TGCAAAATTAACGCTGAGAGCTGAGGACAAGGCTGTGATTAATCACTGTG	AAAAA	424						

RESULT 4				
BF663281				
LOCUS	BF663281	964 bp	mRNA	linear
DEFINITION	602144406.1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297849 5',_			EST 21-DEC-2000

ACCESSION	BF663281
VERSION	BF663281.1
GI	GI:11937163

KEYWORDS EST.

SOURCE ORGANISM	Homo sapiens (human, Homo sapiens)
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REFERENCE
Eularyoca; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 964)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)

COMMENT **Contact: Robert Strausberg, Ph.D.**

Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Straube, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
Plate: LCM152 row: k column: 02
High quality sequence: stop: 693.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:4297849"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using
the following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN					
Query Match	80.9%	Score 274.2:	DB 2:	Length 964:	
Best Local Similarity	95.6%	Pred. No. 1.3e-71;			
Matches 282; Conservative	0;	Mismatches 13;		Indels 0;	Gaps 0

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QY	62	CCTGTGACAGCTCTGTGATTCACTTTGATGATTTATGCATGTCACTGGTTCGGCCAGGCTTC	121
Db	190	CCTGTGACAGCTCTGTGATTCACTTCACTAGACTATGGAGATGACAGGGTCCCGCAGGCTTC	249
QY	122	CAGGCAAGGGGCTGAGTGGGTGGCGAGTTATCATATGATGAGTGAAGTATAAATCTATG	181
Db	250	CAGGCAAGGGGCTGAGTGGGTGGCGAGTTATCATATGATGAGTGAAGTATAAATCTATG	309
QY	182	CAGACTCCGTGAAAGGGCCGATTCAACAATCTCCAGAGCAATTCCAAGAACACGCTGTATC	241
Db	310	CAGACTCCGTGAAAGGGCCGATTCAACAATCTCCAGAGCAATTCCAAGAACACGCTGTATC	369
QY	242	TGCAAAATGAACAGGCTGAGCTGAGGACACAGGCGTGTATTACTGTGGAATAA	296
Db	370	TGCAAAATGAACAGGCTGAGCTGAGGACACAGGCGTGTATTACTGTGGAATAA	424

RESULT 5	LOCUS	DEFINITION
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ACCESSION	BF974524
VERSION	BF974524.1
KEYWORDS	EST.

SOURCE Homo sapiens (human).

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REFERENCE
AUTHORS
1 Mammalia; Butheria; Primates; Catarrhini; Homnidae; Homo.
(bases 1 to 991)
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institute

JOURNAL COMMENT **Unpublished (1999)**
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

FEATURES
 Tissue Procurement: Louis M. Straud, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1204 row: k column: 08
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 Location/Qualifiers

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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN

Query Match	80.9%	Score 274.2	DB 4	Length 991
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Qy	62	CGTGTGCACTCTTGATTCACCTTTGATGATTAAGCAATGCACTGGGTCCGCAAGCTC	121
Db	190	CCGTGCACACTCTGGATTCACTTCACTAGCAATGCAATGCAATGGGTCCGCAAGCTC	249
Qy	122	CAGGCAAGGGGCGTGGATGGGTGGCAGTTATATATATATGATGAGAAATTAATATCTATG	181
Db	250	CAGGCAAGGGGCGTGGATGGGTGGCAGTTATATATATATGATGAGAAATTAATATCTATG	309
Qy	182	CAGACTCCGTGAAGGGCCGATTCAACAATCTCCAGAGCAAAATCCAGAACACGCTGTATC	241
Db	310	CAGACTCCGTGAAGGGCCGATTCAACAATCTCCAGAGCAAAATCCAGAACACGCTGTATC	369
Qy	242	TGCAATATGAACAGCCTGAGAGCTGAGGACACGGCTGTATTAATGTGGCAAAA	296
Db	370	TGCAATATGAACAGCCTGAGAGCTGAGGACACGGCTGTATTAATGTGGCAAAA	424

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
1 (bases 1 to 846)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
 Plate: LCM1707 row: m column: 13
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 Location/Qualifiers

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Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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Query Match	80.6%	Score 273.2	DB 4	Length 846
Best Local Similarity	95.6%	Pred. No. 2.5e-71		
Matches 281; Conservative	0	Mismatches 13	Indels 0	Gaps 0

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Db 130 AGGTGACAGCTGGTGAAGTCTGGGGGAGGCGGTGTCAGCGCTGGAGACTCT 189
Qy 62 CCGTGGACACCTCTGATTCACCTTGATGATTATGCCATGCACTGGGTCGGCCAGGCTC 121
Db 190 CCGTGGACACCTCTGATTCACCTTGATGATTATGCCATGCACTGGGTCGGCCAGGCTC 249
Qy 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAAGTAATAATACTATG 181
Db 250 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAAGTAATAATACTATG 309
Qy 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
Db 310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 369
Qy 242 TGCMAATGAACAGCTGAGAGTGAAGACAGGCTGTGTTACTGTGGGAAA 295
Db 370 TGCMAATGAACAGCTGAGAGTGAAGACAGGCTGTGTTACTGTGGGAAA 423

RESULT 8

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DEFINITION 602713521F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853837 5',
mRNA sequence.
ACCESSION BG756211
VERSION BG756211.1 GI:1406864
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 912)
TITLE NIH-MGC http://mgs.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCMT700 row: i column: 06
High quality sequence stop: 889.
Location/Qualifiers
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FEATURES

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/organism="Homo sapiens"
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/note="Organ: B-cells; Vector: pOT87; Site: 1: XhoI;
Site: 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Query Match 80.4%; Score 272.6; DB 4; Length 912;
Best Local Similarity 95.3%; Pred. No. 3.8e-71;
Matches 281; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 2 AGGTGACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGACTCT 61
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Db 181 CCGTGGACACCTCTGATTCACCTTGATGATTATGCCATGCACTGGGTCGGCCAGGCTC 240
Qy 122 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAAGTAATAATACTATG 181
Db 241 CAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGGAAGTAATAATACTATG 300
Qy 182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
Db 301 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 360
Qy 242 TGCMAATGAACAGCTGAGAGTGAAGACAGGCTGTGTTACTGTGGGAAA 296
Db 361 TGCMAATGAACAGCTGAGAGTGAAGACAGGCTGTGTTACTGTGGGAAA 415

RESULT 9

LOCUS BX344075 413 bp mRNA linear EST 08-APR-2004
DEFINITION BX344075 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1052YB21 5-PRIME, mRNA sequence.
ACCESSION BX344075
VERSION BX344075.2 GI:46279625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 413)
TITLE Li W.B., Gruber C., Jesssee, J. and Polayes D.
JOURNAL Full-length CDNA libraries and normalization
COMMENT On May 2, 2003 this sequence version replaced gi:30342243.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7198.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdnafs-CS1A1013ZH11QPlc=7198.r.
Location/Qualifiers
1..413

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1052YB21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 80.2%; Score 271.8; DB 5; Length 413;
Best Local Similarity 95.2%; Pred. No. 5.6e-71;
Matches 279; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Qy 2 AGGTGACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGACTCT 61
Db 120 AGGTGACAGCTGCTGAGTCTGGGGAGTCTGTGTACAGCTGGGGGCTCCGTGAGACTCT 179
Qy 62 CCGTGGACACCTCTGATTCACCTTGATGATTATGCCATGCACTGGGTCGGCCAGGCTC 121
Db 180 CCGTGGACACCTCTGATTCACCTTGATGATTATGCCATGCACTGGGTCGGCCAGGCTC 239

QY 122 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 181
DB 240 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 299
QY 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 241
DB 300 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 359
QY 242 TGCAATGTAACAGCTTGAGAGCTGAGGACAGGCTGTGTATTACTGTGGGAA 294
DB 360 TGCAATGTAACAGCTTGAGAGCTGAGGACAGGCTGTGTATTACTGTGGGAA 412

RESULT 10
LOCUS AM401728 516 bp mRNA linear EST 16-FEB-2000
DEFINITION UT-HF-BK0-aaf-f-12-0-UT-r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3053711 5', mRNA sequence.
ACCESSION AM401728
VERSION AM401728.1 GI:6920414
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053711"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pRTT3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 79.8%; Score 270.6; DB 2; Length 516;
Best Local Similarity 95.2%; Pred. No. 1.4e-70;
Matches 279; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTCTGAGTCTGGGGAGTGTGACAGCTGGGGGTCCTGAGACTCT 61
DB 132 AGGTGACAGCTCTGAGTCTGGGGAGTGTGACAGCTGGGGGTCCTGAGACTCT 191
QY 62 CCTGTGAGCCTCTGATTCACCTTTGATGATTCAGATGCACTGGGTCCGACAGCTC 121
DB 192 CCTGTGAGCCTCTGATTCACCTTTGATGATTCAGATGCACTGGGTCCGACAGCTC 251
QY 122 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 181
DB 252 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 311

QY 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 241
DB 312 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 371
QY 242 TGCAATGTAACAGCTTGAGAGCTGAGGACAGGCTGTGTATTACTGTGGGAA 294
DB 372 TGCAATGTAACAGCTTGAGAGCTGAGGACAGGCTGTGTATTACTGTGGGAA 424

RESULT 11
LOCUS BQ420418 899 bp mRNA linear EST 23-MAY-2002
DEFINITION AGENCOURT 7827143 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6014112
IMAGE:6014112 5', mRNA sequence.
ACCESSION BQ420418
VERSION BQ420418.1 GI:21115733
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLM13208 Row: b Column: 01
High quality sequence stop: 500.

FEATURES
source location/Qualifiers
1..899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6014112"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 79.5%; Score 269.6; DB 5; Length 899;
Best Local Similarity 99.7%; Pred. No. 3.1e-70;
Matches 281; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTCTGAGTCTGGGGAGTGTGACAGCTGGGGGTCCTGAGACTCT 61
DB 78 AGGTGACAGCTCTGAGTCTGGGGAGTGTGACAGCTGGGGGTCCTGAGACTCT 137
QY 62 CCTGTGAGCCTCTGATTCACCTTTGATGATTCAGATGCACTGGGTCCGACAGCTC 121
DB 138 CCTGTGAGCCTCTGATTCACCTTTGATGATTCAGATGCACTGGGTCCGACAGCTC 197
QY 122 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 181
DB 198 CAGGCAAGGGGCTGAGTGGTGAGCTTATCATATGATGAGTAATAATCTATG 257
QY 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 241
DB 258 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCCAAAGACGCTGTATC 317

QY 242 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAAAGGAG 301
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DB 318 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAGACACAG 377
|||||

RESULT 12
LOCUS BG686759 663 bp mRNA linear EST 01-MAY-2001
DEFINITION 602550729f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763215 5',
mRNA sequence.
ACCESSION BG686759
VERSION BG686759.1 GI:13918156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 663)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM1618 row: 1 column: 08
High quality sequence stop: 659.

FEATURES

source

1..663
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4763215"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH MGC 48"
/note="Organ: B-cells; Vector: pOT7; Site 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.5%; Score 269.4; DB 4; Length 663;
Best Local Similarity 94.6%; Pred. No. 3.3e-70;
Matches 279; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGTAACGCTGGGGGTCCTCGAGACTT 61
|||||
DB 129 AGGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACGCTGGGGGTCCTCGAGACTT 188
|||||
QY 62 CCGTGACGCTCTGATTCACCTTGATGATTATGATGACGCTGGGCGCGCAGGCTC 121
|||||
DB 189 CCGTGACGCTCTGATTCACCTTGATGATTATGATGACGCTGGGCGCGCAGGCTC 248
|||||
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTATG 181
|||||
DB 249 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTATG 308
|||||
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCGCTATTC 241
|||||
DB 309 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCGCTATTC 368
|||||
QY 242 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAAAGGAG 296
|||||

DB 369 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAGAC 423
|||||

RESULT 13
LOCUS AM402572 503 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BKO-aax-b-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055079 5', mRNA sequence.
ACCESSION AM402572
VERSION AM402572.1 GI:6921271
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 503)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

source

1..503
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3055079"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/clone_11b="NIH MGC 36"
/note="Vector: pRTT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafido, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 78.8%; Score 267.2; DB 2; Length 503;
Best Local Similarity 87.0%; Pred. No. 1.4e-69;
Matches 315; Conservative 0; Mismatches 23; Indels 24; Gaps 1;
QY 2 AGGTGAGCTGCTCGAGTCTGGGGAGTGTGTGTAACGCTGGGGGTCCTCGAGACTT 61
|||||
DB 44 AGGTGAGCTGCTGAGTCTGGGGAGTGTGTGTAACGCTGGGGGTCCTCGAGACTT 103
|||||
QY 62 CCGTGACGCTCTGATTCACCTTGATGATTATGATGACGCTGGGCGCGCAGGCTC 121
|||||
DB 104 CCGTGACGCTCTGATTCACCTTGATGATTATGATGACGCTGGGCGCGCAGGCTC 163
|||||
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTATG 181
|||||
DB 164 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTATG 223
|||||
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCGCTATTC 241
|||||
DB 224 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAAACAGCGCTATTC 283
|||||
QY 242 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAAAGGAG 295
|||||
DB 284 TCAGATGAACAGCCCTGAGAGCTGAGACACGCGCTGTATTACTGTGGCAAAAGGAG 343
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QY 296 -----AGGAAGCTACTGGGGCCAGGAAACCTGTGACCGTCTCT 337
DB 344 ATTACGATTTTGGAGTCCACAACACTACTGGGGCCAGGAAACCTGTGACCGTCTCT 403
QY 338 CA 339
DB 404 CA 405

RESULT 14

LOCUS BQ708235 894 bp mRNA linear EST 16-UTL-2002
DEFINITION AGENCOURT_8354494 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281304
5', mRNA sequence.
ACCESSION BQ708235
VERSION BQ708235.1 GI:21847134
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2473 row: 0 column: 01
High quality sequence stop: 585.
Location/Qualifiers

FEATURES

source

1..894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6281304"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 78.7%; Score 266.8; DB 5; Length 894;
Best Local Similarity 92.7%; Pred. No. 2.2e-69;
Matches 280; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTAACGCTGGGGGTCCTCGAAGCT 61
DB 122 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTAACGCTGGGGGTCCTCGAAGCT 181
QY 62 CCGTGACAGCTCTCGATTCACCTTGTGATGATTCAGTCACTGGTCCGCCAGGCTC 121
DB 182 CCGTGACAGCTCTCGATTCACCTTGTGATGATTCAGTCACTGGTCCGCCAGGCTC 241
QY 122 CAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAATAATCTATG 181
DB 242 CAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAATAATCTACG 301
QY 182 CAGACTCGGTGAAGGGCCGATTCACCATCTCCAGAGACAATCCAAAGAACGCTGTATC 241
DB 302 CAGACTCGGTGAAGGGCCGATTCACCATCTCCAGAGACAATCCAAAGAACGCTGTATC 361

QY 242 TGCAAATGAACAGCCTGAGAGTGAAGACAGGCTGTGTATTAATGTCGAAAAAGAG 301
DB 362 TGCAAATGAACAGCCTGAGAGTGAAGACAGGCTGTGTATTAATGTCGAAAAAGAG 421
QY 302 GC 303
DB 422 GC 423

RESULT 15

LOCUS BG503730 456 bp mRNA linear EST 27-MAR-2001
DEFINITION 602549705F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657248 5',
mRNA sequence.
ACCESSION BG503730
VERSION BG503730.1 GI:13465247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1449 row: 1 column: 01
High quality sequence stop: 456.
Location/Qualifiers

FEATURES

source

1..456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4657248"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgccggcgc); Site 2: SfiI (ggccatcagcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATATGAGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGAGGCGCGCAGATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 78.6%; Score 266.6; DB 4; Length 456;
Best Local Similarity 90.7%; Pred. No. 2.1e-69;
Matches 284; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTAACGCTGGGGGTCCTCGAAGCT 61
DB 96 AGGTGACAGCTGCTCGAGTCTGGGGAGTGTGTAACGCTGGGGGTCCTCGAAGCT 155
QY 62 CCGTGACAGCTCTCGATTCACCTTGTGATGATTCAGTCACTGGTCCGCCAGGCTC 121
DB 156 CCGTGACAGCTCTCGATTCACCTTGTGATGATTCAGTCACTGGTCCGCCAGGCTC 215
QY 122 CAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAATAATCTATG 181

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Db      216 CAGGCAAGGGGCTGGAGTGGGTGCGAGTTATATGATGATGAGTAATAAATACTATG 275
QY      182 CAGACTCCGTGAAGGGCCGATTTCACCATCTCCAGAGACAATTCCAAGAACCGCTGTATC 241
Db      276 CAGACTCCGTGAAGGGCCGATTTCACCATCTCCAGAGACAATTCCAAGAACCGCTGTATC 335
QY      242 TGCATAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAAAGSAG 301
Db      336 TGCATAATGAACAGCCTGAGAGCCGAGAGACACGGCTGTATTACTGTGCGAGACACAG 395
QY      302 GCTACTGGGGCCA 314
Db      396 TGAGGGGAGGTCA 408

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Search completed: September 11, 2005, 22:50:37
 Job time : 2730.33 secs

Page Blank (uspio)

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
US-08-545-809A-30

Query Match 80.5%; Score 272.8; DB 3; Length 512;
Best Local Similarity 94.3%; Pred. No. 5.6e-80;
Matches 283; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AGGTGAGGCTGCTCGAGTCTGGGGGAGTGTGTGAGAGCTGGGGGCTCCGAGACTCT 61
DB 169 AGGTGAGGCTGCTGGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGGTCCTGAGACTCT 228
QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 121
DB 229 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 288
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 181
DB 289 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 348
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 241
DB 349 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 408
QY 242 TCCAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTGATTAATCTGCGAAGAAAGAG 301
DB 409 TCCAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTGATTAATCTGCGAAGAAAGAG 468

RESULT 5
US-09-456-090A-59
Sequence 59, Application US/09456090A
Patent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
OTHER INFORMATION: M1-5H
US-09-456-090A-59

Query Match 80.5%; Score 272.8; DB 4; Length 675;
Best Local Similarity 88.9%; Pred. No. 6.4e-80;

Matches 311; Conservative 0; Mismatches 27; Indels 12; Gaps 1;

QY 2 AGGTGAGGCTGCTCGAGTCTGGGGGAGTGTGTGAGAGCTGGGGGCTCCGAGACTCT 61
DB 2 AGGTGAGGCTGCTGGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGGTCCTGAGACTCT 61
QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 121
DB 62 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 241
QY 242 TCCAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTGATTAATCTGCGAAGAAAG--- 298
DB 242 TCCAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTGATTAATCTGCGAAGAAAG--- 298
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGCACTGCTCTCA 339
DB 302 TCAGGTAATTGACTATTGGGGCCAGGGAACCTGTGCACTGCTCTCA 351

RESULT 6
US-09-456-090A-91
Sequence 91, Application US/09456090A
Patent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 91
LENGTH: 675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(675)
OTHER INFORMATION: M2-11H
US-09-456-090A-91

Query Match 80.5%; Score 272.8; DB 4; Length 675;
Best Local Similarity 88.9%; Pred. No. 6.4e-80;
Matches 311; Conservative 0; Mismatches 27; Indels 12; Gaps 1;

QY 2 AGGTGAGGCTGCTCGAGTCTGGGGGAGTGTGTGAGAGCTGGGGGCTCCGAGACTCT 61
DB 2 AGGTGAGGCTGCTGGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGGTCCTGAGACTCT 61
QY 62 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 121
DB 62 CCTGTGACAGCTCTGATTCACCTTTGATGATATGATCCATGCACTGGTCCGCAAGCTTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAATACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGCAAGCTGTATC 241
QY 242 TCCAATGAACAGCTGAGAGCTGAGAGCAAGGCTGTGATTAATCTGCGAAGAAAG--- 298

DB 242 TCGCAATGAAACAGCCGAGAGCCGAGTGTATTAATGAGAGACGGGA 301
QY 299 -----AAGCTACTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 339
DB 302 TCGGGTACTTTGACTATTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 351

RESULT 7
US-09-453-234-59

/ Sequence 59, Application US/09453234
/ Patent No. 6794132
/ GENERAL INFORMATION:
/ APPLICANT: Buechler, Joe
/ APPLICANT: Valkirs, Gunars
/ APPLICANT: Gray, Jeff
/ APPLICANT: Lomborg, Nils
/ APPLICANT: Biosite Diagnostics, Inc.
/ APPLICANT: Genpharm International
/ TITLE OF INVENTION: Human Antibodies
/ FILE REFERENCE: 020015-000110US
/ CURRENT APPLICATION NUMBER: US/09/453,234
/ CURRENT FILING DATE: 1999-12-01
/ PRIOR APPLICATION NUMBER: US 60/157,415
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 59
/ LENGTH: 675
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: M1-5H
/ NAME/KEY: CDS
/ LOCATION: (1)..(675)
US-09-453-234-59

Query Match 80.5%; Score 272.8; DB 4; Length 675;
Best Local Similarity 88.9%; Pred. No. 6.4e-80;
Matches 311; Conservative 0; Mismatches 27; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGCTCGATCTGGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGGAGTGTGGGGGAGCGTGTGTCCAGCTGGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGGATTCACTTTGATGATTAATGATGAGTGGGCTCCGCAAGGCTC 121
DB 62 CCTGTGACGCTCTGGATTCACTTTGATGATGAGTGGGCTCCGCAAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGATTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGATTAATAATACTATG 181
QY 182 CAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 182 CAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
QY 242 TCGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGGAAAAAGG--- 298
DB 242 TCGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGGAAAAAGG--- 298
QY 299 -----AAGCTACTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 339
DB 302 TCGGGTACTTTGACTATTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 351

RESULT 8
US-09-453-234-91
/ Sequence 91, Application US/09453234
/ Patent No. 6794132
/ GENERAL INFORMATION:
/ APPLICANT: Buechler, Joe
/ APPLICANT: Valkirs, Gunars

/ APPLICANT: Gray, Jeff
/ APPLICANT: Lomborg, Nils
/ APPLICANT: Biosite Diagnostics, Inc.
/ APPLICANT: Genpharm International
/ TITLE OF INVENTION: Human Antibodies
/ FILE REFERENCE: 020015-000110US
/ CURRENT APPLICATION NUMBER: US/09/453,234
/ CURRENT FILING DATE: 1999-12-01
/ PRIOR APPLICATION NUMBER: US 60/157,415
/ PRIOR FILING DATE: 1999-10-02
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 91
/ LENGTH: 675
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(675)
/ OTHER INFORMATION: M2-11H
US-09-453-234-91

Query Match 80.5%; Score 272.8; DB 4; Length 675;
Best Local Similarity 88.9%; Pred. No. 6.4e-80;
Matches 311; Conservative 0; Mismatches 27; Indels 12; Gaps 1;

QY 2 AGGTGACGCTGCTCGATCTGGGGGAGTGTGTACAGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGCTGGAGTGTGGGGGAGCGTGTGTCCAGCTGGAGTCCCTGAGACTCT 61
QY 62 CCTGTGACGCTCTGGATTCACTTTGATGATTAATGATGAGTGGGCTCCGCAAGGCTC 121
DB 62 CCTGTGACGCTCTGGATTCACTTTGATGATTAATGATGAGTGGGCTCCGCAAGGCTC 121
QY 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGATTAATAATACTATG 181
DB 122 CAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGATTAATAATACTATG 181
QY 182 CAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
DB 182 CAGACTCCCTGTAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTATC 241
QY 242 TCGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGGAAAAAGG--- 298
DB 242 TCGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTAATCTGTGGAAAAAGG--- 298
QY 299 -----AAGCTACTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 339
DB 302 TCGGGTACTTTGACTATTGGGGCCAGGGAAACCTGGTCAACGCTCCCTCA 351

RESULT 9
US-09-560-198A-1

/ Sequence 1, Application US/09560198A
/ Patent No. 6492497
/ GENERAL INFORMATION:
/ APPLICANT: Thompson, Julia E
/ APPLICANT: Leonard, Simon N
/ APPLICANT: Wilton, Alison J
/ APPLICANT: Braddock, Peter SH
/ APPLICANT: Du Fou, Sarah L
/ APPLICANT: McCafferty, John G
/ APPLICANT: Conroy, Louise A
/ APPLICANT: Tempest, Philip R
/ TITLE OF INVENTION: Specific binding members for Tgfbeta1
/ FILE REFERENCE: 28111/35620A
/ CURRENT APPLICATION NUMBER: US/09/560,198A
/ CURRENT FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/131,983
/ PRIOR FILING DATE: 1999-04-30
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1

LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
US-09-560-198A-1

Query Match
Best Local Similarity 90.9%; Pred. No. 5,5e-80;
Matches 290; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGCTT 61
DB 2 AGGTGACGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGCTT 61
QY 62 CCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 121
DB 62 CCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 121
QY 122 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATATG 181
DB 122 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGATC 241
QY 242 TCGAATGAAACACCTGAGAGCTGAGGACACGGCTGTGTATCTGTGCGAAGAAAGAG 301
DB 242 TCGAATGAAACACCTGAGAGCTGAGGACACGGCTGTGTATCTGTGCGAAGAAAGAG 301
QY 302 GCTACTGGGGCCAGGGAAC 320
DB 302 AATATAGTGGCTACGATAC 320

RESULT 10
US-09-456-090A-55
Sequence 55, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 677
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(677)
OTHER INFORMATION: M1-3H
US-09-456-090A-55

Query Match
Best Local Similarity 80.3%; Score 272.2; DB 4; Length 677;
Matches 311; Conservative 0; Mismatches 28; Indels 12; Gaps 1;

QY 1 GAGTGCAGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGACTC 60
DB 3 GAGTGCAGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGACTC 62
QY 61 TCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 120
DB 61 TCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 120
QY 121 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATAT 180
DB 121 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATAT 180

DB 123 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATAT 182
QY 181 GCAAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGAT 240
DB 183 GCAAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGAT 242
QY 241 CTGCAAAATGAACGCTGAGCTGAGGACACGGCTGTGTATTAATCTGTGCGAAGAAAG-- 298
DB 243 CTGCAAAATGAACGCTGAGGACACGGCTGTGTATTAATCTGTGCGAAGAAAG-- 298
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGTACCCGTCTCTCA 339
DB 303 ATCGGTAATTGACTATTGGGGCCAGGGAACCTGTGTACCCGTCTCTCTCA 353

RESULT 11
US-09-453-234-55
Sequence 55, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 677
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(677)
US-09-453-234-55

Query Match
Best Local Similarity 80.3%; Score 272.2; DB 4; Length 677;
Matches 311; Conservative 0; Mismatches 28; Indels 12; Gaps 1;

QY 1 GAGTGCAGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGACTC 60
DB 3 GAGTGCAGCTGCTGAGTCTGGGAGTCTGTGTACAGCTGGGGGCTCCCTGAGACTC 62
QY 61 TCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 120
DB 61 TCTGTGACGCTCTGTGATTTACCTTGTATATGCAAGCACTGGTCCGCAAGCTT 122
QY 121 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATAT 180
DB 121 CAGGCAAGGGGCTGAGTGGTGGAGTTATCATATGATGGAAGTAATTAATCATAT 182
QY 181 GCAAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGAT 240
DB 183 GCAAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGCAATTCGAAGAACCGCTGAT 242
QY 241 CTGCAAAATGAACGCTGAGCTGAGGACACGGCTGTGTATTAATCTGTGCGAAGAAAG-- 298
DB 243 CTGCAAAATGAACGCTGAGGACACGGCTGTGTATTAATCTGTGCGAAGAAAG-- 298
QY 299 -----AAGCTACTGGGGCCAGGGAACCTGTGTACCCGTCTCTCA 339
DB 303 ATCGGTAATTGACTATTGGGGCCAGGGAACCTGTGTACCCGTCTCTCTCA 353


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Db      59 AGGTGACGCTGTGAGTCTGGGGGAGGCGTGTGAGGCTGGAGAGTCCCTGAGACTCT 118
Qy      62 CCTGTGACGCTTGTGATTCACCTTTGATGATTATATGCATGCACTGGGTCGCCGAGGCTC 121
Db      119 CCTGTGACGCTTGTGATTCACCTTTGATGATTATATGCATGCACTGGGTCGCCGAGGCTC 178
Qy      122 CAGGCAAGGGGCTGAGTGGGTCGAGTTATATCATATGATGGAAGTAATAATATATG 181
Db      179 CAGGCAAGGGGCTGAGTGGGTCGAGTTATATGATGGAAGTAATAATACTATG 238
Qy      182 CAGACTCCGCTGAGAGGCGCCATTCCACCATCTCCAGAGCAATTCCAGAAACGCTGTATC 241
Db      239 CAGACTCCGCGAAGGGCCGATTCCACCATCTCCAGAGCAATTCCAGAAACGCTGTATC 298
Qy      242 TGCAGATGAACAGCTGAGAGCTGAGAGCAACGCTGTATTACTGTGCGAAAAAGAA- 300
Db      299 TGCAGATGAACAGCTGAGAGCCGAGAGCAACGCTGTATTACTGTGCGAGAGCCGAGAC 358
Qy      301 -----GGCTACTGGGGCCAGGGAACCTGGTCAACGCTCTCTCA 339
Db      359 TCCTGGGTTACTTTGACTACTGGGGCCAGGGAACCTGGTCAACGCTCTCTCA 411

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RESULT 15
US-09-472-087-59
; Sequence 59, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-Pf1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-59

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Query Match      80.1%; Score 271.4; DB 4; Length 1392;
Best Local Similarity 88.4%; Pred. No. 2.6e-79;
Matches 312; Conservative 0; Mismatches 26; Indels 15; Gaps 1;

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Qy      2 AGGTGACGCTGTGAGTCTGGGGGAGTGTGATGAGGCTGGGGGTCCTTGAGACTCT 61
Db      59 AGGTGACGCTGTGAGTCTGGGGGAGGCGTGTGAGGCTGGAGAGTCCCTGAGACTCT 118
Qy      62 CCTGTGACGCTTGTGATTCACCTTTGATGATTATGCAATGCACTGGGTCGCCGAGGCTC 121
Db      119 CCTGTGACGCTTGTGATTCACCTTTGATGATTATGCAATGCACTGGGTCGCCGAGGCTC 178
Qy      122 CAGGCAAGGGGCTGAGTGGGTCGAGTTATATCATATGATGGAAGTAATAATATATG 181
Db      179 CAGGCAAGGGGCTGAGTGGGTCGAGTTATATGATGGAAGTAATAATACTATG 238
Qy      182 CAGACTCCGCTGAGAGGCGCCATTCCACCATCTCCAGAGCAATTCCAGAAACGCTGTATC 241
Db      239 CAGACTCCGCGAAGGGCCGATTCCACCATCTCCAGAGCAATTCCAGAAACGCTGTATC 298
Qy      242 TGCAGATGAACAGCTGAGAGCTGAGAGCAACGCTGTATTACTGTGCGAAAAAGAA- 300
Db      299 TGCAGATGAACAGCTGAGAGCCGAGAGCAACGCTGTATTACTGTGCGAGAGCCGAGAC 358

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Qy      301 -----GGCTACTGGGGCCAGGGAACCTGGTCAACGCTCTCTCA 339
Db      359 TCCTGGGTTACTTTGACTACTGGGGCCAGGGAACCTGGTCAACGCTCTCTCA 411

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OM nucleic - nucleic search, using sw model

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- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	339	100.0	372	US-10-325-694-145	Sequence 145, App
2	301.2	88.8	729	US-10-406-830-20	Sequence 20, Appl
3	294.8	87.0	396	US-10-309-764-54	Sequence 54, Appl
4	289.2	85.3	342	US-10-738-120-9	Sequence 9, Appl1
5	285.2	84.1	537	US-10-805-177-25	Sequence 25, Appl1
6	284.4	83.9	357	US-10-010-729-8	Sequence 8, Appl1
7	284	83.8	352	US-10-638-265-17	Sequence 17, Appl

8	283.8	83.7	405	17	US-10-309-764-58	Sequence 58, Appl
9	282	83.2	783	19	US-10-642-120-5	Sequence 5, Appl1
10	282	83.2	783	19	US-10-642-060-5	Sequence 5, Appl1
11	282	83.2	783	19	US-10-642-122-5	Sequence 5, Appl1
12	282	83.2	783	19	US-10-642-124-5	Sequence 5, Appl1
13	282	83.2	783	19	US-10-621-269-5	Sequence 5, Appl1
14	282	83.2	783	19	US-10-620-950-5	Sequence 5, Appl1
15	282	83.2	783	20	US-10-642-118-5	Sequence 5, Appl1
16	282	83.2	783	20	US-10-642-119-5	Sequence 5, Appl1
17	282	83.2	783	20	US-10-642-117-5	Sequence 5, Appl1
18	282	83.2	783	20	US-10-642-099-5	Sequence 5, Appl1
19	282	83.2	783	20	US-10-642-064-5	Sequence 5, Appl1
20	282	83.2	783	21	US-10-642-116-5	Sequence 5, Appl1
21	282	83.2	783	21	US-10-642-100-5	Sequence 5, Appl1
22	282	83.2	783	21	US-10-642-058-5	Sequence 5, Appl1
23	282	83.2	783	21	US-10-642-121-5	Sequence 5, Appl1
24	282	83.2	783	22	US-10-642-065-5	Sequence 5, Appl1
25	282	83.2	783	22	US-10-642-071-5	Sequence 5, Appl1
26	282	83.2	783	22	US-10-642-059-5	Sequence 5, Appl1
27	280.6	82.8	349	18	US-10-269-711-18	Sequence 18, Appl
28	280.6	82.8	349	19	US-10-684-109-18	Sequence 18, Appl
29	280.6	82.8	404	17	US-10-309-764-74	Sequence 74, Appl
30	280.6	82.8	405	17	US-10-309-764-70	Sequence 70, Appl
31	279	82.3	405	17	US-10-309-764-66	Sequence 66, Appl
32	277.4	81.8	405	17	US-10-309-764-62	Sequence 62, Appl
33	276.8	81.7	414	15	US-10-325-694-143	Sequence 143, App
34	276.6	81.6	369	21	US-10-625-307A-7	Sequence 7, Appl1
35	276.2	81.5	397	9	US-09-878-178-2106	Sequence 2106, Ap
36	276.2	81.5	397	13	US-10-046-935-2106	Sequence 2106, Ap
37	276.2	81.5	397	14	US-10-146-502-2106	Sequence 2106, Ap
38	275.8	81.4	405	17	US-10-309-764-78	Sequence 78, Appl
39	275.8	81.4	405	17	US-10-309-764-138	Sequence 138, App
40	275	81.1	345	21	US-10-625-307A-5	Sequence 5, Appl1
41	275	81.1	345	21	US-10-625-307A-60	Sequence 60, Appl
42	275	81.1	350	21	US-10-625-307A-36	Sequence 36, Appl
43	274.6	81.0	354	15	US-10-324-493-7	Sequence 7, Appl1
44	274.6	81.0	366	21	US-10-727-155-13	Sequence 33, Appl
45	274.4	80.9	376	17	US-10-292-088-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-10-325-694-145
; Sequence 145, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPFER, PETER
; APPLICANT: RAJIM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 372
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-145

Query Match 100.0%; Score 339; DB 15; Length 372;

Best Local Similarity 100.0%; Pred. No. 2e-102;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGTGACGCTGCTGAGCTTGGGGAGCTGCTGATACGCTTGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACGCTGCTGAGCTTGGGGAGCTTGGGGAGCTTGGGGGTCCCTGAGACTC 60

NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 342
TYPE: DNA
ORGANISM: Homo sapiens
US-10-738-120-9

Query Match 85.3%; Score 289.2; DB 20; Length 342;
Best Local Similarity 92.6%; Pred. No. 7.8e-86;
Matches 315; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61
DB 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61
QY 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCACTGGCTGGGCTCCGAGGCTC 121
DB 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCACTGGCTGGGCTCCGAGGCTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATCATATGATGAAATTAATAACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATGATGAAATTAATAACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCAACATCTCAGAGACAATTCCAAGAACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCAACATCTCAGAGACAATTCCAAGAACGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGCTGAGACACAGCTGTGTATTAATCTGTGC--GAAAAAGGA 299
DB 242 TGCATATGAACAGCTGAGAGCTGAGACACAGCTGTGTATTAATCTGTGTGAGAGATACCTT 301
QY 300 AGGCTACTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 339
DB 302 TGACTACTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 341

RESULT 5
US-10-805-177-25

Sequence 25, Application US/10805177
Publication No. US20050084449A1
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Binyam
APPLICANT: Foltz, Ian
APPLICANT: Tse, Kam Fai
APPLICANT: Jeffers, Michael
APPLICANT: Meiri, Mehdi
APPLICANT: Starling, Gary
APPLICANT: Mezes, Peter
APPLICANT: Khramtsov, Nikolai
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
FILE REFERENCE: ABXCUR.006A
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/456,652
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 537
TYPE: DNA
ORGANISM: Homo sapiens
US-10-805-177-25

Query Match 84.1%; Score 285.2; DB 21; Length 537;
Best Local Similarity 90.2%; Pred. No. 2e-84;
Matches 305; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61
DB 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61

DB 2 AGTGCAGCTGAGAGAGTGGGGGGAGGCGTGTCCAGCCTGGAGAGTCCCTGAGACTCT 61
QY 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCAATGCACTGGGTCGGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCAATGCACTGGGTCGGCCAGGCTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATCATATGATGAAATTAATAACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATGATGAAATTAATAACTATG 181
QY 182 CAGACTCCGTGAAGGGCCGATTCAACATCTCAGAGACAATTCCAAGAACGCTGTATC 241
DB 182 CAGACTCCGTGAAGGGCCGATTCAACATCTCAGAGACAATTCCAAGAACGCTGTATC 241
QY 242 TGCATATGAACAGCTGAGAGCTGAGACACAGCTGTGTATTAATCTGTGTGAGAGAG 301
DB 242 TGCATATGAACAGCTGAGAGCTGAGACACAGCTGTGTATTAATCTGTGTGAGAGAG 301
QY 302 GCTACTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 339
DB 302 ACTACTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 339

RESULT 6
US-10-010-729-8

Sequence 8, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
FILE REFERENCE: 1199-1-005CIP2
CURRENT FILING DATE: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 357
TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-729-8

Query Match 83.9%; Score 284.4; DB 16; Length 357;
Best Local Similarity 90.4%; Pred. No. 3.2e-84;
Matches 322; Conservative 0; Mismatches 16; Indels 18; Gaps 1;

QY 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61
DB 2 AGTGCAGCTGCTCGAGTCTGGGGAGTGTGTGTAAGGCTGGGGGTCCTCGAGACTCT 61
QY 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCAATGCACTGGGTCGGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGGATTCACTTTGATGATTATGCAATGCACTGGGTCGGCCAGGCTC 121
QY 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATCATATGATGAAATTAATAACTATG 181
DB 122 CAGGCAAGGGGCTGGAGTGGGTGGGTCAGTATATCATATGATGAAATTAATAACTATG 181

Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 1 GAGGTGCAGCTCTGCAAGTCTGGGGAGTCGTGTACACCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGCAGCTGTGAGTCTGGGGAGGCGTGTCCACCTGGGGGGTCCCTGAGACTC 78
QY 61 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 120
DB 79 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 138

QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 198

QY 181 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 240
DB 199 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 258

QY 241 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAAGAA 300
DB 259 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAGATTGCAT 318

QY 301 GGCTA---CTGGGGCCAGGGAACCTGTGTACCGCTCTC 335
DB 319 GCTCAGACTTGGGGCCAAAGGTACCTGTGTACCGCTCTC 356

RESULT 10
US-10-642-060-5
; Sequence 5, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorne, Philip E.
; APPLICANT: Soares, M. Melina
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibod
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 783
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-10-642-060-5

Query Match 83.2%; Score 282; DB 19; Length 783;
Best Local Similarity 91.7%; Pred. No. 2.6e-83;
Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 1 GAGGTGCAGCTCTGCAAGTCTGGGGAGTCGTGTACACCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGCAGCTGTGAGTCTGGGGAGGCGTGTCCACCTGGGGGGTCCCTGAGACTC 78
QY 61 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 120
DB 79 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 138

QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 198

QY 181 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 240
DB 199 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 258

QY 241 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAAGAA 300
DB 259 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAGATTGCAT 318

QY 301 GGCTA---CTGGGGCCAGGGAACCTGTGTACCGCTCTC 335
DB 319 GCTCAGACTTGGGGCCAAAGGTACCTGTGTACCGCTCTC 356

QY 241 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAAGAA 300
DB 259 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAGATTGCAT 318

QY 301 GGCTA---CTGGGGCCAGGGAACCTGTGTACCGCTCTC 335
DB 319 GCTCAGACTTGGGGCCAAAGGTACCTGTGTACCGCTCTC 356

RESULT 11
US-10-642-122-5
; Sequence 5, Application US/10642122
; Publication No. US20040131622A1
; GENERAL INFORMATION:
; APPLICANT: Thorne, Philip E.
; APPLICANT: Soares, M. Melina
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using
; FILE REFERENCE: 3999.002985
; CURRENT APPLICATION NUMBER: US/10/642,122
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 783
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-10-642-122-5

Query Match 83.2%; Score 282; DB 19; Length 783;
Best Local Similarity 91.7%; Pred. No. 2.6e-83;
Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 1 GAGGTGCAGCTCTGCAAGTCTGGGGAGTCGTGTACACCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGCAGCTGTGAGTCTGGGGAGGCGTGTCCACCTGGGGGGTCCCTGAGACTC 78
QY 61 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 120
DB 79 TCTGTGCAGCTCTGTGATTCACCTTGTATGATTTATGATCCATGACATGCGGTCGCGAGGCT 138

QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTTATATCATATGATGAAAGTAATAATATCTAT 198

QY 181 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 240
DB 199 GGAAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAATTCGAAGAACGCTGTAT 258

QY 241 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAAGAA 300
DB 259 CTGCAAAATGAAACAGCTGAGAGCTGAGACACGGCTGTATTTACTGTGCAAAAGATTGCAT 318

QY 301 GGCTA---CTGGGGCCAGGGAACCTGTGTACCGCTCTC 335
DB 319 GCTCAGACTTGGGGCCAAAGGTACCTGTGTACCGCTCTC 356

RESULT 12
US-10-642-124-5
; Sequence 5, Application US/10642124
; Publication No. US20040161429A1
; GENERAL INFORMATION:
; APPLICANT: Thorne, Philip E.
; APPLICANT: Soares, M. Melina

```
APPLICANT: Ran, Sophia
TITLE OF INVENTION: Compositions for Treating Viral Infections Using Immunoconjugates
FILE REFERENCE: 3999.002984
CURRENT APPLICATION NUMBER: US/10/642,124
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 10/621,269
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,263
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 783
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-10-642-124-5
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Query Match 83.2%; Score 282; DB 19; Length 783;
Best Local Similarity 91.7%; Pred. No. 2.6e-83;
Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

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QY 1 GAGGTGACGCTCTGAGTCTG3GGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGACGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGGAGTCCCTGAGACTC 78
QY 61 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 120
DB 79 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 138
QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 198
QY 181 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 240
DB 199 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 258
QY 241 CTGCAATGAACAGCTGAGAGTGAAGACAGGGCTGTATTTACTGTGCGAAAAAGAA 300
DB 259 CTGCAATGAACAGCTGAGAGTGAAGACAGGGCTGTATTTACTGTGCGAAATTGCAT 318
QY 301 GGCTA---CTGGGGCCAGGGAACCTTGATCACCGTCTC 335
DB 319 GCTCAGACTTGGGGCCAGGTAACCTTGATCACCGTCTC 356
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RESULT 13
US-10-621-269-5
Sequence 5, Application US/10621269
Publication No. US20040170620A1
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Ran, Sophia
TITLE OF INVENTION: Selected Antibody Compositions for Binding to Aminophospholipids
FILE REFERENCE: 4001.003000
CURRENT APPLICATION NUMBER: US/10/621,269
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,263
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 783
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-10-621-269-5
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Query Match 83.2%; Score 282; DB 19; Length 783;

Best Local Similarity 91.7%; Pred. No. 2.6e-83;
Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

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QY 1 GAGGTGACGCTCTGAGTCTG3GGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGACGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGGAGTCCCTGAGACTC 78
QY 61 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 120
DB 79 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 138
QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 198
QY 181 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 240
DB 199 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 258
QY 241 CTGCAATGAACAGCTGAGAGTGAAGACAGGCTGTATTTACTGTGCGAAAAAGAA 300
DB 259 CTGCAATGAACAGCTGAGAGTGAAGACAGGCTGTATTTACTGTGCGAAATTGCAT 318
QY 301 GGCTA---CTGGGGCCAGGGAACCTTGATCACCGTCTC 335
DB 319 GCTCAGACTTGGGGCCAGGTAACCTTGATCACCGTCTC 356
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RESULT 14
US-10-620-850-5
Sequence 5, Application US/10620850
Publication No. US20040175378A1
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Ran, Sophia
TITLE OF INVENTION: Selected Antibody Compositions and Methods for Binding to
FILE REFERENCE: 4001.003082
CURRENT APPLICATION NUMBER: US/10/620,850
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,263
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 09/613,430
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 783
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-10-620-850-5
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Query Match 83.2%; Score 282; DB 19; Length 783;
Best Local Similarity 91.7%; Pred. No. 2.6e-83;
Matches 310; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

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QY 1 GAGGTGACGCTCTGAGTCTG3GGAGTCTGTGTACAGCTGGGGGGTCCCTGAGACTC 60
DB 19 GAGGTGACGCTGTGAGTCTGGGGAGGCGTGTCCAGCTGGGAGTCCCTGAGACTC 78
QY 61 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 120
DB 79 TCTGTGACGCTCTGAGATTCACTTTGATGATATGATCCATGACTGGTCCGCAAGCT 138
QY 121 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 180
DB 139 CCAGGCAAGGGGCTGAGTGGTGGGAGTATATATATATGAGTAAGTAATAATACTAT 198
QY 181 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 240
DB 199 GCAGACTCCGTGAAGGCCGATTCACATCTCCAGAGCAATTCACAGACGCTGTAT 258
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Oy	241	CTGCAAAATGAAAGAGCTGAGCTGATGGAACAAGGCTGTATATCTGTCGAAAAAGGAA	300
Db	259	CTGCAAAATGAAAGAGCTGAGCTGATGGAACAAGGCTGTATATCTGTCGAAATTGCAT	318
Oy	301	GAGTA---CTGGGCGCAGGGAACCTGTGTACCGGTCTC	335
Db	319	GCTCAGACTTGGGGCCAAAGTACCCGTGTACCGGTCTC	356

RESULT 15

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US-10-642-118-5
: Sequence 5, Application US/10642118
: Publication No. US20040208668A1
: GENERAL INFORMATION:
: APPLICANT: Thorpe, Philip E.
: APPLICANT: Ram, Sophia
: TITLE OF INVENTION: Selected Antibody CDRs for Binding to Aminophospholipids
: FILE REFERENCE: 4001.003085
: CURRENT APPLICATION NUMBER: US/10/642,118
: CURRENT FILING DATE: 2003-08-15
: PRIOR APPLICATION NUMBER: US 10/621,269
: PRIOR FILING DATE: 2003-07-15
: PRIOR APPLICATION NUMBER: 60/396,263
: PRIOR FILING DATE: 2002-07-15
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 783
: TYPE: DNA
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
: US-10-642-118-5

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Query Match	83.2%;	Score 283;	DB 20;	Length 783;
Best Local Similarity	91.7%;	Pred. No. 2.6e-83;		
Matches 310;	Conservative	0;	Mismatches 25;	Indels 3;
				Gaps 1;

Search completed: September 12, 2005, 02:01:32
Job time : 539.75 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 18:03:37 ; Search time 1629.32 Seconds
(without alignments)
9546.401 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 ggagccagatgacccagc.....ggagcagctggacattcaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Genemdb1:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_dr:*
10: gb_ro:*
11: gb_stb:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	6	A84380 Sequence 14
2	321	100.0	321	6	BD075296 Novel met
3	321	100.0	1630	6	BD222938 Heteromln
4	321	100.0	1630	6	BD222939 Heteromln
5	321	100.0	1630	6	AX023365 Sequence
6	321	100.0	1630	6	AX023367 Sequence
7	260.2	81.1	321	6	A84374
8	260.2	81.1	321	6	BD139668 A novel m
9	260.2	81.1	321	6	AX003761 Sequence
10	260.2	81.1	321	6	BD075293 Novel met
11	245.8	76.6	324	6	BD187178 Human-tyr
12	245.8	76.6	324	6	BD187179 Human-tyr
13	244.2	76.1	339	9	AB006842 Homo sapi
14	244.2	76.1	342	6	BD097614 Anticbody
15	242.6	75.6	321	6	BD097618 Anticbody
16	242.6	75.6	814	9	AB064076 Homo sapi
17	241	75.1	315	9	HSFAB82VL
18	240.8	75.0	318	12	AF044455 Synthetic
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21	237.8	74.1	324	6	AX112586 Sequence
22	237.8	74.1	735	6	CO832185 Sequence
23	237	73.8	324	9	AB095290 Homo sapi
24	236.2	73.6	321	6	A29589 H.sapiens c
25	236.2	73.6	324	12	AF538696 Synthetic
26	236.2	73.6	642	9	AB095273 Homo sapi
27	236.2	73.6	1000	9	HSVK01 X00965 Human reart
28	235.6	73.4	324	9	HS1G311 X79786 H.sapiens (
29	234.6	73.1	612	9	H0M1GKAE K02135 Human Ig ac
30	234.6	73.1	642	9	AB030640 Homo sapi
31	234.4	73.0	936	6	BD248703 Immunoglo
32	233	72.6	324	9	HSVUTEL9 X61642 Human Ig re
33	233	72.6	450	9	AF103775 Homo sapi
34	232.8	72.5	917	6	BD248694 Immunoglo
35	231.8	72.2	384	9	HSFOW016 Z68992 H.sapiens m
36	231.4	72.1	324	9	AB063929 Homo sapi
37	231.4	72.1	333	6	BD097236 X94431 H.sapiens r
38	231.4	72.1	346	9	HS61B61GK AJ548508 Homo sapi
39	231.4	72.1	388	9	HS4548508 C0761230 Sequence
40	231.4	72.1	720	6	CO761230 Sequence
41	231.4	72.1	720	6	CO840583 Sequence
42	231.4	72.1	720	6	AR476229 Sequence
43	231.4	72.1	720	6	AX740176 Sequence
44	231.4	72.1	720	6	BD077368 Method of
45	231.4	72.1	761	9	AB064051 Homo sapi

ALIGNMENTS

RESULT 1	A84380	Sequence 147 from Patent WO9846645.	321 bp	DNA	linear	PAT 21-JAN-2000
LOCUS	A84380					
DEFINITION	A84380					
ACCESSION	A84380.1	GI:6733303				
VERSION						
KEYWORDS						
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 321)					
AUTHORS	Kuifer P. and Raum T.					
TITLE	NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND USES THEREOF					
JOURNAL	Patent: WO 9846645-A 147 22-OCT-1998;					
FEATURES	KUFER PETER (DE); RAUM TORIAS (DE)					
source	Location/Qualifiers					
	1..321					
	/organism="unidentified"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32644"					
	<1..>321					
	/note="unnamed protein product"					
	/codon_start=1					
	/protein_id="CAB69290.1"					
	/db_xref="GI:6733304"					
	/translation="ELQMTQSPSSISASVGRVTITTCRASGISISLYLNMVQKPGQP					
	KLIYMASTRSGVDPFSGSGSGTNYLTITLSIQPEDFATYFCQSDSLITFGQT					
	RLDIQ"					
ORIGIN						
Query Match	100.0%; Score 321; DB 6;					
Best Local Similarity	100.0%; Pred. No. 2.3e-97;					
Matches 321; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTGAGAGACAGATCAC	60			
DB	1	GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGTGAGAGACAGATCAC	60			
QY	61	ATCACTTCGCGGCGGCAAGTCAGAGCATTTAGAGCATTTAAATTGGTATCAGCAGAACCA	120			
DB	61	ATCACTTCGCGGCGGCAAGTCAGAGCATTTAGAGCATTTAAATTGGTATCAGCAGAACCA	120			

QY 121 GGACAGCCTCTTAAGTGTGCTATTCTAGGAGCATACCGGGAAATCGGGGTCCTGAC 180
DB 121 GGACAGCCTCTTAAGTGTGCTATTCTAGGAGCATACCGGGAAATCGGGGTCCTGAC 180
QY 181 CGATTGAGGGGAGGATCTGAGCAAAATTACACTCTGACATGAGAGCCTGAGCCT 240
DB 181 CGATTGAGGGGAGGATCTGAGCAAAATTACACTCTGACATGAGAGCCTGAGCCT 240
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTTTGCCGATCACTTGCCGCA 300
DB 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTTTGCCGATCACTTGCCGCA 300
QY 301 GGGACAGCACTGGACATTCGA 321
DB 301 GGGACAGCACTGGACATTCGA 321

RESULT 2
BD075296
LOCUS BD075296
DEFINITION Novel method for the production of anti-human antigen receptors and uses thereof.
ACCESSION BD075296
VERSION BD075296.1 GI:22620899
KEYWORDS JP 2001519824-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Kufer,P. and Raum,T.
TITLE Novel method for the production of anti-human antigen receptors and uses thereof
JOURNAL Patent: JP 2001519824-A 25 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/25
PD 23-OCT-2001
PR 14-APR-1998 JP 1998543494
PI 14-APR-1997 EP 97106109.8
PC C07K16/00,C07K16/30,A61K39/395
CC Novel method for the production of anti-human antigen CC
receptors and uses
CC thereof
FH Key
FT CDS Location/Qualifiers
1..321 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.3e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 CGATTGAGGGGAGGATCTGAGCAAAATTACACTCTGACATGAGAGCCTGAGCCT 240
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTTTGCCGATCACTTGCCGCA 300
DB 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTTTGCCGATCACTTGCCGCA 300
QY 301 GGGACAGCACTGGACATTCGA 321
DB 301 GGGACAGCACTGGACATTCGA 321

RESULT 3
BD222938
LOCUS BD222938
DEFINITION Heteromnibodies.
ACCESSION BD222938
VERSION BD222938.1 GI:33032708
KEYWORDS JP 2002521053-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
TITLE Heteromnibodies
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN Mus musculus (mouse)
PS JP 2002521053-A/32
PD 16-JUL-2002
PR 28-JUL-1999 JP 2000562401
PI 28-JUL-1998 EP 9814082.5
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,
PI FLORIAN ZETTL
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
PC C07K19/00,
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53//C12N5/10,C12R1:91,
PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
PC (C12N5/00,C12R1:91)
CC Heteromnibodies
FH Key
FT CDS Location/Qualifiers
1..1630 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 321; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCTGTCGATCTGTAGAGAGAGTCAAC 60
DB 96 GAGCTCCAGATGAGCCAGTCTCCATCTCTGTCGATCTGTAGAGAGAGTCAAC 155
QY 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTTAAATTGGTATCAGCAAAACA 120
DB 156 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTTAAATTGGTATCAGCAAAACA 215
QY 121 GAGAGCCTCCCTAACTGCTATTCTAGGAGATCTACCCGGGAATCCGGGGTCCCTAC 180
DB 216 GAGAGCCTCCCTAACTGCTATTCTAGGAGATCTACCCGGGAATCCGGGGTCCCTAC 275
QY 181 CGATTGAGGGGAGGATCTGAGCAAAATTACACTCTGACATGAGAGCCTGAGCCT 240
DB 276 CGATTGAGGGGAGGATCTGAGCAAAATTACACTCTGACATGAGAGCCTGAGCCT 335
QY 241 GAAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGATTTTGCCGATCACTTGCCGCA 300

Db 336 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGGCAA 395

QY 301 GGGACACGACTGGACATTCAA 321

Db 396 GGGACACGACTGGACATTCAA 416

RESULT 4

BD222939

LOCUS BD222939 1630 bp DNA linear PAT 17-JUL-2003

DEFINITION Heteromnibodies.

ACCESSION BD222939

VERSION BD222939.1 GI:33032709

KEYWORDS JP 2002521053-A/33.

SOURCE JP 2002521053-A/33.

ORGANISM Homo sapiens (human)

REFERENCE 1 Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F. Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Heteromnibodies Patent: JP 2002521053-A 33 16-JUL-2002; MICROMET AG

COMMENTS OS Homo sapiens (human) OS Mus musculus (mouse) PN JP 2002521053-A/33 PD 16-JUL-2002 JP 2000562401 PP 28-JUL-1999 JP 2000562401 PR 28-JUL-1998 EP 98114082.5 P1 PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN BORSCHERT, PI FLORIAN ZETTL, PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02, PC C07K19/00, PC C12N5/10,C12P21/02,G01N33/53,G01N33/53// (C12N5/10,C12R1.91), PC (C12P21/02,C12R1.91),C12N15/00,C12N5/00,A61K37/02,A61K37/66, PC (C12N5/00,C12R1.91) CC Heteromnibodies FH Key Location/Qualifiers FT CDS Location/Qualifiers

1..1630 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 321; DB 6; Length 1630; Best Local Similarity 100.0%; Pred. No. 2.5e-97; Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGATCACC 60

Db 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGATCACC 155

QY 61 ATACCTTCCCGGCAAGTCAAGACATTAAGCTATTAATGTGATGACGAAACCA 120

Db 156 ATACCTTCCCGGCAAGTCAAGACATTAAGCTATTAATGTGATGACGAAACCA 215

QY 121 GAGACGCTCTTAAGCTGTCTATTTACTGGGATCTAACCGGGAATCCGGGTCCTGAC 180

Db 216 GAGACGCTCTTAAGCTGTCTATTTACTGGGATCTAACCGGGAATCCGGGTCCTGAC 275

QY 181 CGATTCAAGCGGAGTGAATCTGGACAATTAACCTCTCAATCAAGACAGCTGACCT 240

Db 276 CGATTCAAGCGGAGTGAATCTGGACAATTAACCTCTCAATCAAGACAGCTGACCT 335

QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGGCAA 300

Db 336 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGGCAA 395

QY 301 GGGACACGACTGGACATTCAA 321

Db 396 GGGACACGACTGGACATTCAA 416

RESULT 5

AX023365

LOCUS AX023365 1630 bp DNA linear PAT 15-SEP-2000

DEFINITION Sequence 36 from Patent WO0006605.

ACCESSION AX023365

VERSION AX023365.1 GI:10183777

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE 1 Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K. Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Heteromnibodies Patent: WO 0006605-A 36 10-FEB-2000; KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ; BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GRS FUER BIOMEDIZINIS (DE) Location/Qualifiers

1..1630 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 39..1610 /note="unnamed protein product" /codon_start=1 /protein_id="CAC08835.1" /db_xref="GI:10183778" /translation="MGNSCIITFLVATANGVSEUOMTSPSSLSASVDRVITICRA SOSISITLAWIQKRPDPKILITVASTRESVPPRFGSESGITVTLTSLQEDF ATYFQGDSDLEITFGQGTSLDIQGGSGSGGSGSGSEVQLLEGGGVVPGRSILR LSCAAGSFSTFSGVHMWROAPGKLBWAVISYDGSNKYVADSVKGFPTISRDSKN TLYLQMSLRADPDAVYVCAQMGWGSGRPYVYGMVWGQGVTVVSSGTPLDIT HTASTKPSVFPFLADSSKSTSGTAAAGLVDPPEPVYVWNSGALTSVHTPPAV LOSGLYSLSSVTVVPSSTSGTQYICVNHKBSMTKVDKVEPSCKMTSGGGSAP AASBPSTQPMFHVNAIOPARLILSLSDPTAEKMEYTVVISMFDLQEPFLQRLB LYKGLRSLTSLTKGPLTMWASHYKQHPPEPPTSCATQIITFESFKENLKDFLIVP FDCWEPVQEHHHHHH"

ORIGIN

Query Match 100.0%; Score 321; DB 6; Length 1630; Best Local Similarity 100.0%; Pred. No. 2.5e-97; Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGATCACC 60

Db 96 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGATCACC 155

QY 61 ATACCTTCCCGGCAAGTCAAGACATTAAGCTATTAATGTGATGACGAAACCA 120

Db 156 ATACCTTCCCGGCAAGTCAAGACATTAAGCTATTAATGTGATGACGAAACCA 215

QY 121 GAGACGCTCTTAAGCTGTCTATTTACTGGGATCTAACCGGGAATCCGGGTCCTGAC 180

Db 216 GAGACGCTCTTAAGCTGTCTATTTACTGGGATCTAACCGGGAATCCGGGTCCTGAC 275

QY 181 CGATTCAAGCGGAGTGAATCTGGACAATTAACCTCTCAATCAAGACAGCTGACCT 240

Db 276 CGATTCAAGCGGAGTGAATCTGGACAATTAACCTCTCAATCAAGACAGCTGACCT 335

QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGGCAA 300

Db 336 GAAGATTTTGTCTACTTCTTGTCAACAGTGTGACAGTTTGGCGATCACTTGGGCAA 395

QY 301 GGGACACGACTGGACATTCAA 321

Db 396 GGGACACGACTGGACATTCAA 416

RESULT 6

AX023367	LOCUS	AX023367	1630 bp	DNA	linear	PAT 15-SEP-2000
LOCUS	Sequence 38 from Patent WO0006605.					
DEFINITION	AX023367					
ACCESSION	AX023367.1	GI:10183779				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
JOURNAL	1					
	Kuifer, P., Zettl, F., Dreier, T., Bauearle, P.A. and Borschert, K.					
	Heteromindobates					
	Patent: WO 0006605-A 38 10-FEB-2000;					
	KUFR PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;					
	BAUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER					
	BIOMEDIZINIS (DE)					
FEATURES						
SOURCE	Location/Qualifiers					
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	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
	39..1613					
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	/codon_start=1					
	/protein_id="CAC08836.1"					
	/db_xref="gi:10183780"					
	/translation="MGMSCLILFPAATGATGSHLOMTQSPSSLSAGVDRVITTCBRA					
	SQSLSYLAWYQOKGQPKLLIYWAATRESGVDRPFGSSGSGNYTLTSLQPEDP					
	ATYQCDQDLSPIPTFGQCTRLDIOGGSSGGGGGGGGGSEVQLLESGGVQVPRSLR					
	LSCAAGCTFTSFGMHWRAQPGKGLEVAVISTDGSNKRYADSVKGRFTISRDNSK					
	TLVLYQMSLRAEDTAAVYYCAQDMQSGWREPYYYGMDVQGTIVVSQTPLDGDTT					
	HTRVAAAPSVPIPPSPDEQLKSGTASVVCILNNFYPRPAKQVMDVALQSGNSQSV					
	TEQSKDSYSLSTLTLSKADYEKHVYACEVTHQGLSPTVSKFNKSGSGGSGSA					
	PTSSSTKTOLOLPHLLDLMIIINGINNYKQPKLTNLTPEKFMKPAETELKLOCCI					
	EEELKPLEEVNLAQSKPHLRPRDLISNINVIYELKSGSETTMCERYADETATIVER					
	LNRWITTFQSLITLT"					
ORIGIN						
Query Match	100.0%; Score 321; DB 6; Length 1630;					
Best Local Similarity	100.0%; Pred. No. 2,5e-97;					
Matches 321; Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 GAGCTCCAGATGATGCCAGCTCTCCATCTCCTGCTGCACTGTAGAGACAGATCAC	60				
DB	96 GAGCTCCAGATGATGCCAGCTCTCCATCTCCTGCTGCACTGTAGAGACAGATCAC	155				
OY	61 ATCACTTCCCGGCAAGTCAGAGCACTTATGACAGCTTAAATTTGGTATCAGCAAAACCA	120				
DB	156 ATCACTTCCCGGCAAGTCAGAGCACTTATGACAGCTTAAATTTGGTATCAGCAAAACCA	215				
OY	121 GGACAGCTCTCCTTAAGCTGCTCATTTAATCTAGGGGATCTACCCGGGAAATCCGGGGTCCCTGAC	180				
DB	216 GGACAGCTCTCCTTAAGCTGCTCATTTAATCTAGGGGATCTACCCGGGAAATCCGGGGTCCCTGAC	275				
OY	181 CGATTCAAGCGGAGTGAATCTGGGCAAAATTACACTCTCACATCAGCAGGCTGCAAGCT	240				
DB	276 CGATTCAAGCGGAGTGAATCTGGGCAAAATTACACTCTCACATCAGCAGGCTGCAAGCT	335				
OY	241 GAAGATTTTGGTACTACTTTTGTCAACAGCTGACAGCTTTGGCATTAACCTTGGGCCCA	300				
DB	336 GAAGATTTTGGTACTACTTTTGTCAACAGCTGACAGCTTTGGCATTAACCTTGGGCCCA	395				
OY	301 GGAGACAGCTGACATTTCAA 321					
DB	396 GGAGACAGCTGACATTTCAA 416					
RESULT 7						
AB4374	AB4374	321 bp	DNA	linear	PAT 21-JAN-2000	
LOCUS	Sequence 141 from Patent WO9846645.					
DEFINITION	AB4374					
ACCESSION						

VERSION	A84374.1	GI:6733297
KEYWORDS	unidentified	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 321)	
AUTHORS	Kufner,P. and Raum,T.	
TITLE	NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND USES THEREOF	
JOURNAL	Patent: WO 9846645-A 141 22-OCT-1998;	
FEATURES	KUFER PETER (DB); RAUM TOBIAS (DE)	
source	Location/Qualifiers	
CDS	1..321	
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	/mol_type="unassigned DNA"	
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	<1..>.321	
	/note="unnamed protein product"	
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	/protein_id="CAB69287.1"	
	/db_xref="GI:6733298"	
	/translation="ELCMQSPSSLSASVDRAVTTTCRTSQSISSLYLWYQKRGQPP KLILYMASTRESGVPRFSGSGSTDTPLTLLISLPDASATYYCQGSYDIPIYFRGQGT KLEIK"	
ORIGIN		
Query Match	81.1%; Score 260.2; DB 6; Length 321;	
Best Local Similarity	88.2%; Pred. No. 1e-76;	
Matches	283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;	
OY	1 GAGCTCCAGATGACCCAGTCTCCATTCCTCCCTGTCGTGCATTTGTAGAGACAGAGTGACC 60	
Db	1 GAGCTCCAGATGACCCAGTCTCCATTCCTCCCTGTCGTGCATTTGTAGAGACAGAGTGACC 60	
OY	61 ATCACTGGCGGGGAAGTCAGAGATTAGACAGCATTAATTAATGTTATTCAGACAAGAACA 120	
Db	61 ATCACTGGCGGGGAAGTCAGAGATTAGACAGCATTAATTAATGTTATTCAGACAAGAACA 120	
OY	121 GGACAGCCTCTTAAGTGTCTCATTTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180	
Db	121 GGACAGCCTCTTAAGTGTCTCATTTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180	
OY	181 CGATTACAGCGGCAAGTGAATCTGGGACAATTACACTCTCACCATCAGACGCCCTGCAGCT 240	
Db	181 CGATTACAGTGCACAGCGGTCGGGACAGATTCACTCAACCATCAGACAGCTCAAACT 240	
OY	241 GAAGATTTTGTACTTCACTTTTGTCAACAGCTCAGACAGTTGGCCATCACCTTGAGGCAA 300	
Db	241 GAAGATTTTGTCACTTACTTACTGTACAGACAGATTACAGACATCCGTACACTTTTGGCCAG 300	
OY	301 GGACACAGCACTGACATTCGA 321	
Db	301 GGACCAACAGCTGGAGATCAAA 321	
RESULT 8		
LOCUS	BD139668	
DEFINITION	BD139668 321 bp DNA linear PAT 18-SEP-2002	
ACCESSION	BD139668	
VERSION	BD139668.1 GI:23234613	
KEYWORDS	JP 2002508924-A/53.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Kufner,P., Raum,T., Borschert,K., Zetcl,F. and Iwterbuene,R. A novel method of identifying binding site domains that retain the capacity of binding to an epitope Patent: JP 2002508924-A 53 -MAR-2002;	
JOURNAL	PETER KUFER	

COMMENT OS Homo sapiens (human)
PN JP 2002508924-A/53
PD 26-MAR-2002 JP 2000521184
PF 16-NOV-1998 JP 1998543494
PI 17-NOV-1997 EP 97120096.9
PI PETER KUFER, TOBIAS RAUM, KATRIN BORSCHERT, FLORIAN ZETTL, RALF LUTTERBUESSE
PC C07K16/00, A61K38/00, A61K38/22, A61K38/43, A61K39/395, C07K14/705, C07K16/30, C12N15/09, A61K38/00, A61K38/22, A61K38/43, A61K39/395, C07K14/705, C12N1/21, C12N5/10, C12P21/02, C12P21/08, G01N33/566, C12N15/00, PC A61K37/02,
PC A61K37/24, A61K37/48, C12N5/00
CC A novel method of identifying binding site domains that retain
CC the
CC capacity of binding to an epitope
FH key Location/Qualifiers
FT source 1..321
FT Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 81.1%; Score 260.2; DB 6; Length 321;
Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

ORIGIN

RESULT 9
AX003761 321 bp DNA linear PAT 24-AUG-2000
LOCUS Sequence 55 from Patent WO9925818.
DEFINITION AX003761
ACCESSION AX003761
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity of binding to an epitope
JOURNAL Patent: WO 9925818-A 55 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
Location/Qualifiers

source 1..321
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 81.1%; Score 260.2; DB 6; Length 321;
Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

ORIGIN

RESULT 10
BD075293 321 bp DNA linear PAT 27-AUG-2002
LOCUS Novel method for the production of anti-human antigen receptors and uses thereof.
DEFINITION BD075293
ACCESSION BD075293.1 GI:22620896
VERSION JP 2001519824-A/22.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Kufer, P. and Raum, T.
TITLE Novel method for the production of anti-human antigen receptors and uses thereof
JOURNAL Patent: JP 2001519824-A 22 23-OCT-2001;
MICROMET AG

COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/22
PD 23-OCT-2001 JP 1998543494
PF 14-APR-1998 JP 1998543494
PI 14-APR-1997 EP 97106109.8
PI PETER KUFER, TOBIAS RAUM
PC C07K16/00, C07K16/30, A61K39/395
CC Novel method for the production of anti-human antigen CC receptors and uses
CC thereof
FH key Location/Qualifiers
FT CDS (1)..(321).
FT Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 81.1%; Score 260.2; DB 6; Length 321;

Best Local Similarity 88.2%; Pred. No. 1e-76;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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DB 121 GGACAGCCTCTTAAGCTGCTCATTTTACTGAGGCACTGACCCGGGAATCGGGGTCCTGAC 180
QY 181 CGATTTCAGGGGCAAGTCAAGTGGGCAAAATTACACTCTACCATCAGCAGCTTCAGCCT 240
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QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300
DB 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300
QY 301 GGGACACGACTGACATTCGA 321
DB 301 GGGACACGACTGACATTCGA 321

RESULT 11
BD187178 324 bp DNA linear PAT 17-JUN-2003

LOCUS BD187178 Human-typed antibody against blood coagulation factor VIII.
DEFINITION BD187178.1 GI:31879467
ACCESSION MO 02101040-A/7.
VERSION MO 02101040-A/7.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 324)
AUTHORS Nakashima,T. and Yuguchi,M.
TITLE Human-typed antibody against blood coagulation factor VIII
JOURNAL Patent: WO 02101040-A 7 19-DEC-2002;
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
TOSHIHIRO NAKASHIMA,MASATO YUGUCHI

COMMENT OS Homo sapiens (human)
PN MO 02101040-A/7
PD 19-DEC-2002
PF 11-JUN-2002 MO 2002JP005783
PR 12-JUN-2001 JP 01P 177640
PT TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
PC C12N15/09,C07K16/14,C07K7/06,C07K7/08,C12P21/08,G01N33/53 CC
Human-typed antibody against blood coagulation factor VIII FH Key

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DB 61 ATCACTTGGCGGGCAAGTCAAGACATTAGACAGTATTTAAATTGGTATCAGAGAAACA 120
QY 121 GGACAGCCTCTTAAGCTGCTCATTTTACTGAGGCACTGACCCGGGAATCGGGGTCCTGAC 180
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QY 181 CGATTTCAGGGGCAAGTCAAGTGGGCAAAATTACACTCTACCATCAGCAGCTTCAGCCT 240
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QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300
DB 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300
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DB 301 GGGACACGACTGACATTCGA 321

RESULT 12
BD187179 324 bp DNA linear PAT 17-JUN-2003

LOCUS BD187179 Human-typed antibody against blood coagulation factor VIII.
DEFINITION BD187179.1 GI:31879468
ACCESSION MO 02101040-A/8.
VERSION MO 02101040-A/8.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 324)
AUTHORS Nakashima,T. and Yuguchi,M.
TITLE Human-typed antibody against blood coagulation factor VIII
JOURNAL Patent: WO 02101040-A 8 19-DEC-2002;
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
TOSHIHIRO NAKASHIMA,MASATO YUGUCHI

COMMENT OS Homo sapiens (human)
PN MO 02101040-A/8
PD 19-DEC-2002
PF 11-JUN-2002 MO 2002JP005783
PR 12-JUN-2001 JP 01P 177640
PT TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
PC C12N15/09,C07K16/14,C07K7/06,C07K7/08,C12P21/08,G01N33/53 CC
Human-typed antibody against blood coagulation factor VIII FH Key

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Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 85.4%; Pred. No. 8e-72;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGCTCCATCTCTCTGTGCACTGTGTAGAGACAGAGTCAAC 60
DB 1 GAGCTCCAGATGACCCAGCTCCATCTCTCTGTGCACTGTGTAGAGACAGAGTCAAC 60
QY 61 ATCACTTGGCGGGCAAGTCAAGACATTAGACAGTATTTAAATTGGTATCAGAGAAACA 120
DB 61 ATCACTTGGCGGGCAAGTCAAGACATTAGACAGTATTTAAATTGGTATCAGAGAAACA 120
QY 121 GGACAGCCTCTTAAGCTGCTCATTTTACTGAGGCACTGACCCGGGAATCGGGGTCCTGAC 180
DB 121 GGACAGCCTCTTAAGCTGCTCATTTTACTGAGGCACTGACCCGGGAATCGGGGTCCTGAC 180
QY 181 CGATTTCAGGGGCAAGTCAAGTGGGCAAAATTACACTCTACCATCAGCAGCTTCAGCCT 240
DB 181 CGATTTCAGGGGCAAGTCAAGTGGGCAAAATTACACTCTACCATCAGCAGCTTCAGCCT 240
QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300
DB 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCCGATCACTTCGAGCA 300

QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTGTGACAGTTGGCCGATCACTTGGGCCAA 300
 DB 241 GAAGATTTTGTCACTACTTCTGTCAACAGATTACAGTACCCCGATCACTTGGGCCAA 300
 QY 301 GGGACACGACTGGACATTCAA 321
 DB 301 GGGACACGACTGGACATTCAA 321
 RESULT 13
 LOCUS AB006842 339 bp mRNA linear pri 09-sep-1997
 DEFINITION Homo sapiens mRNA for HRV Fab N6-VL, partial cde.
 ACCESSION AB006842
 VERSION AB006842.1 GI:2385484
 KEYWORDS HRV Fab N6-VL.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Itoh, K. and Suzuki, T.
 TITLE Human anti-rotavirus Fab
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 339)
 AUTHORS Itoh, K.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-1997) Kunihiko Itoh, Akita University Hospital,
 Pharmaceutical Science, Hondo 1-1-1, Akita, Akita 010, Japan
 (E-mail: itohk@hos.akita-u.ac.jp, Tel: +81-188-34-1111,
 Fax: +81-188-36-2628)
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 /db_xref="taxon:9606"
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 /db_xref="GI:2385485"
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 Query Match 76.1%; Score 244.2; DB 9; Length 339;
 Best Local Similarity 85.0%; Pred. No. 2.8e-71;
 Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

DB 307 GGGACACGACTGGACATTCAA 327
 RESULT 14
 LOCUS BD097614 342 bp DNA linear PAT 27-AUG-2002
 DEFINITION Antibody library.
 ACCESSION BD097614
 VERSION BD097614.1 GI:22643188
 KEYWORDS WO 0162907-A/69.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 342)
 AUTHORS Kurosawa, Y., Akahori, Y., Iba, Y., Morino, K., Shinohara, M.,
 Takahashi, M., Okuno, Y. and Shiraki, K.
 TITLE Antibody library
 JOURNAL Patient: WO 0162907-A 69 30-AUG-2001;
 MEDICAL & BIOLOGICAL LABORATORIES CO LTD, YOSHITAKU KUROSAWA,
 YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO MORINO, MIDORI SHINOHARA,
 MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU SHIRAKI
 OS Homo sapiens (human)
 PN WO 0162907-A/69
 PD 30-AUG-2001
 PF 22-FEB-2001 WO 2001JP001298
 PR 22-FEB-2000 JP 00P 50543
 PI YOSHITAKU KUROSAWA, YASUSHI AKAHORI, YOSHITAKA IBA, KAZUHIKO PI
 MORINO,
 PI MIDORI SHINOHARA, MOTOHIDE TAKAHASHI, YOSHINOBU OKUNO, KIMIYASU
 SHIRAKI
 PC C12N15/09, C07K16/00//C12P21/08
 CC Antibody library
 FH Key
 FT source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="Genomic DNA"
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 ORIGIN
 Query Match 76.1%; Score 244.2; DB 6; Length 342;
 Best Local Similarity 85.0%; Pred. No. 2.8e-71;
 Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 17:46:48 ; Search time 337, 536 Seconds
(without alignments)
5629.725 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneeqn1990s:*

3: geneeqn2000s:*

4: geneeqn2001s:*

5: geneeqn2001as:*

6: geneeqn2002as:*

7: geneeqn2002bs:*

8: geneeqn2003as:*

9: geneeqn2003bs:*

10: geneeqn2003cs:*

11: geneeqn2003ds:*

12: geneeqn2004as:*

13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	321	100.0	321	2	AAV68539
2	321	100.0	1630	3	AAZ50588
3	321	100.0	1630	3	AAZ50587
4	260.2	81.1	321	2	AAV68536
5	260.2	81.1	321	2	AAV77237
6	249	77.6	321	11	ADO51603
7	245.8	76.1	324	4	AAH47727
8	244.2	75.6	321	4	AAH47727
9	242.6	75.6	321	5	AAH68651
10	240.8	75.0	321	5	AAH68651
11	240.8	75.0	321	9	ACD45315
12	240.2	74.8	321	12	ADO36505
13	240.2	74.8	321	12	ADO36497
14	238.6	74.3	327	10	ADD89879
15	238.6	74.3	327	13	ADS64655
16	238.6	74.3	327	13	ADS64655
17	237.8	74.1	321	12	ADP22249
18	237.8	74.1	321	12	ADP22249
19	237.8	74.1	735	13	ADR28103
20	236.2	73.6	321	11	ADO51602

21	236.2	73.6	321	12	ADP22235	ADP22235 Human ant
22	236.2	73.6	321	12	ADP22253	ADP22253 Human ant
23	236.2	73.6	458	12	ADK52349	ADK52349 Human ant
24	235	73.2	1106	6	ABQ54241	ABQ54241 Human ova
25	234.4	73.0	936	3	AAA27390	AAA27390 Human IGF
26	233	72.6	321	12	ADP22243	ADP22243 Human ant
27	232.8	72.5	917	3	AAA27381	AAA27381 Human IGF
28	231.4	72.1	333	5	AAH74684	AAH74684 Nucleotid
29	231.4	72.1	333	10	ABT34320	ABT34320 Hepatitis
30	231.4	72.1	720	2	AAK36070	AAK36070 DNA encod
31	231.4	72.1	720	10	ABZ76706	ABZ76706 Human ser
32	231.4	72.1	720	12	ADL92368	ADL92368 Human pha
33	231.4	72.1	720	12	ADQ71166	ADQ71166 HSA Heavy
34	231.4	72.1	900	5	AAH74688	AAH74688 Nucleotid
35	231.4	72.1	900	10	ABT34324	ABT34324 Hepatitis
36	229.8	71.6	321	9	AAZ57375	AAZ57375 Human SFL
37	229.8	71.6	324	10	AAI52120	AAI52120 Human ant
38	229.8	71.6	396	2	AAV75423	AAV75423 Human ant
39	229.8	71.6	684	4	AAH30052	AAH30052 TRO005 Ka
40	229.8	71.6	720	10	ABT34315	ABT34315 Hepatitis
41	229.8	71.6	729	3	AAI11630	AAI11630 Human Imm
42	229.8	71.6	729	6	ABL46009	ABL46009 Humanized
43	228.2	71.1	321	11	ADO51601	ADO51601 Human TAG
44	228.2	71.1	324	4	AAF29086	AAF29086 Human HIV
45	228.2	71.1	324	4	AAF29073	AAF29073 Human HIV

ALIGNMENTS

RESULT 1	AAV68539	standard; DNA, 321 BP.
ID	AAV68539	
AC	AAV68539;	
XX		
DT	16-FEB-1999	(first entry)
XX		
DE	Nucleotide sequence of human kappa 5.1 light chain variable region.	
XX		
KW	Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;	
KV	auto-immune disease; graft rejection; allergy; inflammatory disease;	
KX	endocrine disease; degenerative disease; ss.	
OS	Homo sapiens.	
XX		
FI	Key	Location/Qualifiers
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FT		/product= "human kappa 5.1 light chain variable region"
XX		
PN	WO9846645-A2.	
XX		
PD	22-OCT-1998.	
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PP	14-APR-1998;	98WO-EP002180.
XX		
PR	14-APR-1997;	97EP-00106109.
XX		
PA	(KUPF/) KUPF P.	
XX	(RAUM/) RAUM T.	
XX		
PI	Kufex P, Raum T;	
XX		
DR	WPI, 1998-594564/50.	
XX	P-PSDB; AAV68539.	
PT	Production of anti-human antigen receptors - by selecting a combination	
XX	of functionally rearranged VH and VL immunoglobulin chains expressed from	
PS	a recombinant vector.	
XX	Claim 9; Fig 9; 84pp; English.	

CC This is the nucleotide sequence of the human kappa light chain variable
CC region, used in the method of the invention, for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.5e-93;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTGTAAGAGACAGAGTCAAC 60
DB 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTGTAAGAGACAGAGTCAAC 60
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATCAGCAAGAACCA 120
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DB 121 GGAAGAGCTCTCAAGCTGCTCAATTTACTGGGCAATCAACCGGAAATCCGGGGTCCCTGAC 180
QY 181 CGATTTCAGGGGAGGAGATCTGGGCAATTAACACTCAGCATCAGACAGCTGACAGCT 240
DB 181 CGATTTCAGGGGAGGAGATCTGGGCAATTAACACTCAGCATCAGACAGCTGACAGCT 240
QY 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCCACTTCCGCCCA 300
DB 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCCACTTCCGCCCA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGACATTCAA 321

RESULT 2
AAZ50588
ID AAZ50588 standard; DNA; 1630 BP.
XX
AC AAZ50588;
XX
DT 23-MAY-2000 (first entry)
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DE HD70scFv-Ck-interleukin 2 encoding DNA.
XX
XX HD70; single-chain variable fragment; scFv; 17-1A antigen; human; BpCAM;
XX epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
XX interleukin-2; Ck-domain; kappa light chain constant domain;
XX heteromultimer; multifunctional compound; immunoglobulin; cytostatic;
XX immunostimulatory; antileukemia; diagnosis; prevention;
XX antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
XX leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT misc_feature 96..842
FT /*tag= b
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XX
XX WO200006605-A2.
XX
XX 10-FEB-2000.
XX
XX 28-JUL-1999; 99WO-EP005416.

XX 28-JUL-1998; 98EP-00114082.
XX
XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baenerle PA, Borschert K, Zettl F;
XX WPI; 2000-195265/17.
XX P-PEDB; AAY44995.
XX
XX New multifunctional compounds useful for preventing and/or treating
XX malignant cell growth and for detection and diagnosis.
XX
XX Claim 8; Fig 55B; 166pp; English.

CC The patent discloses heteromultimers which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises a C₁-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteromultimers have
CC cytostatic, immunostimulatory, antileukemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding right
CC chain of a heteromultimer comprising HD70 single-chain Fv (scFv) fragment
CC N-terminally linked to human Ck domain (constant domain of immunoglobulin
CC -kappa light chain) which bears at its C-terminus the human inflammatory
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 321; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.8e-93;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTGTAAGAGACAGAGTCAAC 60
DB 96 GAGCTCCAGATGACCCAGTCTCCATCCCTGCTGCTGTAAGAGAGACAGAGTCAAC 155
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DB 156 ATCACTTGGCCGGGCAAGTCAAGACATTAAGCACTATTAAATTGGTATCAGCAAGAACCA 120
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DB 121 GGAAGAGCTCTCAAGCTGCTCAATTTACTGGGCAATCAACCGGAAATCCGGGGTCCCTGAC 180
QY 216 GGAAGAGCTCTCAAGCTGCTCAATTTACTGGGCAATCAACCGGAAATCCGGGGTCCCTGAC 275
DB 216 GGAAGAGCTCTCAAGCTGCTCAATTTACTGGGCAATCAACCGGAAATCCGGGGTCCCTGAC 275
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DB 216 CGATTTCAGGGGAGGAGATCTGGGCAATTAACACTCAGCATCAGACAGCTGACAGCT 240
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DB 241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTCCGATCCACTTCCGCCCA 300
QY 301 GGGACACGACTGGACATTCAA 321
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QY 396 GGGACACGACTGGACATTCAA 416
DB 396 GGGACACGACTGGACATTCAA 416

RESULT 3
AAZ50587
ID AAZ50587 standard; DNA; 1630 BP.
XX
AC AAZ50587;
XX


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XX SQ Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other:
Query Match 81.1%; Score 260.2; DB 2; Length 321;
Best Local Similarity 88.2%; Pred. No. 7.5e-74;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 1 GAGCTCCAGATGACCAAGTCTCCATCCCTGCTGCTGATGAGAGACAGATCAC 60
DB 1 GAGCTCCAGATGACCAAGTCTCCATCCCTGCTGCTGATGAGAGACAGATCAC 60
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OY 241 GAAAGTTTGTCTACTTCTTTGCAACAGTCTGACAGTTTCCGATCACCTTGGCCCA 300
DB 241 GAAAGTTTGTCTACTTCTTTGCAACAGTCTGACAGTTTCCGATCACCTTGGCCCA 300
OY 301 GGGACACGACTGACATTCAA 321
DB 301 GGGACACGACTGAGATCAA 321

RESULT 5
AAK77237
ID AAK77237 standard; DNA; 321 BP.
XX AAK77237;
XX
XX 04-AUG-1999 (first entry)
XX
XX Human kappa 8 light chain variable region encoding DNA.
XX
XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX autoimmune disease; scFv-antibody; single-chain Fv; ss.
XX
XX Homo sapiens.
XX
XX WO925818-A1.
XX
XX 27-MAY-1999.
XX
XX 16-NOV-1998; 98WO-EP007313.
XX
XX 17-NOV-1997; 97EP-00120096.
XX
XX (KUFE/) KUFER P.
XX
XX Kufer P, Raum T, Borschert K, Zetl F, Lutterbuese R;
XX
XX WPI, 1999-338004/28.
XX
XX P-PSDB; AAY17955.
XX
XX Phase display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX
XX Disclosure; Fig 3.2; 152pp; English.
XX
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
```

```
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method
XX
XX SQ Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other:
Query Match 81.1%; Score 260.2; DB 2; Length 321;
Best Local Similarity 88.2%; Pred. No. 7.5e-74;
Matches 283; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 1 GAGCTCCAGATGACCAAGTCTCCATCCCTGCTGCTGATGAGAGACAGATCAC 60
DB 1 GAGCTCCAGATGACCAAGTCTCCATCCCTGCTGCTGATGAGAGACAGATCAC 60
OY 61 ATCACTTCCGGGCGGCAAGTCAAGACATTAGACAGCTAATTAATGATACAGAAACCA 120
DB 61 ATCACTTCCGGGCGGCAAGTCAAGACATTAGACAGCTAATTAATGATACAGAAACCA 120
OY 121 GAGACAGCTCTTAAGCTGCTATTAATCTGGGATCCCGGGATCCCTGAC 180
DB 121 GAGACAGCTCTTAAGCTGCTATTAATCTGGGATCCCGGGATCCCTGAC 180
OY 181 CGATTCAAGCGGAGTGAATCTGGGCAAAATTACACTCTCAGCATGACAGCTGAGCCT 240
DB 181 CGATTCAAGCGGAGTGAATCTGGGCAAAATTACACTCTCAGCATGACAGCTGAGCCT 240
OY 241 GAAAGTTTGTCTACTTCTTTGCAACAGTCTGACAGTTTCCGATCACCTTGGCCCA 300
DB 241 GAAAGTTTGTCTACTTCTTTGCAACAGTCTGACAGTTTCCGATCACCTTGGCCCA 300
OY 301 GGGACACGACTGACATTCAA 321
DB 301 GGGACACGACTGAGATCAA 321

RESULT 6
AD051603
ID AD051603 standard; DNA; 321 BP.
XX AD051603;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human TAG-72 antibody-related KCS18 gene SeqID13.
XX
XX semi-human monoclonal antibody; tumour-associated glycoprotein antigen;
XX TAG-72; human light chain; cancer; AKA; HxK; VKI;
XX human immunoglobulin kappa light chain germline; gene; ds; human.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..321
XX /tag= a
XX /product= "Human TAG-72 antibody-related KCS18 protein"
XX /partial
XX /note= "No start or stop codon"
XX
XX KR2003013633-A.
XX
XX 15-FEB-2003.
XX
XX 08-AUG-2001; 2001KR-00047737.
XX
XX 08-AUG-2001; 2001KR-00047737.
```


XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 PA Hong HJ, Kim SJ;
 PI WPI; 2003-500992/47.
 DR P-PSDB; ADO51598.
 XX
 PT Semi-human monoclonal antibody binding to tumor-associated glycoprotein
 PT antigen tag-72 and human light chain comprising the same, useful for
 PT diagnosing and treating cancer.
 PS Claim 13; SEQ ID NO 18; 1bp; Korean.
 XX
 CC This invention relates to a novel semi-human monoclonal antibody binding
 CC to tumor-associated glycoprotein antigen TAG-72 and a human light chain
 CC comprising the same. The semi-human monoclonal antibody has a human light
 CC chain of which amino acid sequence is completely derived from the human,
 CC therefore it is useful for the diagnosis and treatment of cancer. The
 CC semi-human monoclonal antibody specifically binds to TAG-72 antigen of
 CC which the light chain of human antibody AKA/HZK is substituted with the
 CC light chain of a human derived antibody. The light chain of the human
 CC derived antibody is preferably composed of amino acid sequence derived
 CC from the V λ family of the human immunoglobulin kappa light chain
 CC germline. The present sequence is that of a gene which encodes a human
 CC KCS protein which is related to the novel semi-human TAG-72 antibody of
 CC the invention.
 XX
 SQ Sequence 321 BP; 87 A; 86 C; 73 G; 75 T; 0 U; 0 Other;

Query Match 77.6%; Score 249; DB 11; Length 321;
 Best Local Similarity 86.0%; Pred. No. 3.2e-70;
 Matches 276; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTACC 60
 DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTACC 60
 QY 61 ATCACTTCCGCGGCAAGTACAGGATTAAGTATTAATGATAGCAGAAACCA 120
 DB 61 ATCACTTCCGCGGCAAGTACAGGATTAAGTATTAATGATAGCAGAAACCA 120
 QY 121 GAGACGCTCTTAAGCTGCTCATTTACTGGGATCTACCCGGGATCCGGGTCCTGAC 180
 DB 121 GAGAAAGCCCCCTAAGTCTGATCTATAAGGATCTAGTAAGAGTGGGATCCATCA 180
 QY 181 CGATTCAGCGGAGTGAATCTGGGACAAATTACACTCTCAGATCAGACGCTGACGCT 240
 DB 181 AGGTTCAAGCGGAGTGAATCTGGGACAAATTACACTCTCAGATCAGACGCTGACGCT 240
 QY 241 GAAAGATTTGCTACTTACTTTGTCAACGCTGAGAGTTTGGCATCCTTTGGCCAA 300
 DB 241 GATGATTTTGGTACTTATTACTGTCAACAGACTTACATGATGCCCCCATCTTCGGCCAA 300
 QY 301 GGGACGAGCTGGACATTCAA 321
 DB 301 GGGACGAGCTGGAGATTAAA 321

RESULT 7
 AAL52122
 ID AAL52122 standard; DNA; 324 BP.

XX AAL52122;
 AC AAL52122;
 XX
 DT 29-MAY-2003 (first entry)
 XX
 DE Human anti-blood coagulation factor VIII antibody-related gene #4.
 XX
 KW Human; gene; db; anti-blood coagulation factor VIII antibody;
 KW FVIII antibody; anti-thrombotic; thrombosis; activated FVIII.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 1..324
 FT CDS
 FT /*tag= a
 FT /partial
 FT /product= "Human VIII antibody-related protein #4"
 FT /note= "No start or stop codon is given"

PN WO2002101040-A1.

PD 19-DEC-2002.

PF 11-JUN-2002; 2002WO-JP005783.

PK 12-JUN-2001; 2001JP-00177640.

PA (KAGA) CHERO-SERO-THERAPEUTIC RES INST.

PI Nakashima T, Yuguichi M;

DR WPI; 2003-148804/14.

DR P-PSDB; AAO16706.

PT Human-type anti-blood coagulation factor VIII antibody, applicable in
 PT antithrombotics for prevention or treatment of thrombosis, in diagnosis
 PT of activated FVIII, and for maintaining low coagulation state.

PS Disclosure; Page 28; 39pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a human
 CC anti-blood coagulation factor VIII (FVIII) antibody, which has an
 CC inhibitory activity on the coagulation activity of human FVIII. The
 CC antibody is applicable in anti-thrombotics for prevention or treatment of
 CC thrombosis, and in the diagnosis of activated FVIII. The present DNA
 CC sequence encodes a human FVIII antibody-related protein

SQ Sequence 324 BP; 87 A; 88 C; 73 G; 76 T; 0 U; 0 Other;

Query Match 76.6%; Score 245.8; DB 10; Length 324;
 Best Local Similarity 85.4%; Pred. No. 3.5e-69;
 Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTACC 60
 DB 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGAGACAGAGTACC 60
 QY 61 ATCACTTCCGCGGCAAGTACAGGATTAAGTATTAATGATAGCAGAAACCA 120
 DB 61 ATCACTTCCGCGGCAAGTACAGGATTAAGTATTAATGATAGCAGAAACCA 120
 QY 121 GAGACGCTCTTAAGCTGCTCATTTACTGGGATCTACCCGGGAAATCCGGGTCCTGAC 180
 DB 121 GGGAAAGCCCCCTAAGCTCTGATCTATCTGATCTCAATGCAAGTGGGGTCCATCA 180
 QY 181 CGATTCAGCGGAGTGAATCTGGGACAAATTACACTCTCAGATCAGACGCTGACGCT 240
 DB 181 AGGTTCAAGCGGAGTGAATCTGGGACAAATTACACTCTCAGATCAGACGCTGACGCT 240
 QY 241 GAAAGATTTGCTACTTACTTTGTCAACGCTGAGAGTTTGGCATCCTTTGGCCAA 300
 DB 241 GAAAGATTTTGGCACTTACTTACTGTCAACAGAGTTACAGATACCCGATCACCCTGGCCAA 300
 QY 301 GGGACGAGCTGGACATTCAA 321
 DB 301 GGGACGAGCTGGAGATTAAA 321

RESULT 8
 AAH47727
 ID AAH47727 standard; DNA; 342 BP.

XX AAH47727;
 AC AAH47727;
 XX

```
DT 30-NOV-2001 (first entry)
XX Nucleotide sequence of seq Id No. 70.
DE Gene library; immunoglobulin; antibody library; human; ds.
XX Homo sapiens.
XX MO200162907-A1.
XX 30-AUG-2001.
XX 22-FEB-2001; 2001WO-JP001298.
XX 22-FEB-2000; 2000JP-00050543.
XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX MPI; 2001-565420/63.
DR P-PSDB; AAG65563.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
XX Examples; p 146-147; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
XX Sequence 342 BP; 91 A; 93 C; 78 G; 80 T; 0 U; 0 Other;
SQ
Query Match 76.1%; Score 244.2; DB 4; Length 342;
Best Local Similarity 85.0%; Pred. No. 1.2e-68;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCTGTCTGATCTGTAGAGACAGAGTACC 60
DB 1 GACATCGTATGACCCAGTCTCCATCTCCTGTCTGATCTGTAGAGACAGAGTACC 60
QY 61 ATCACTTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGAGAAACCA 120
QY 121 GGACAGCCTCTTAAGTCTGCTCATTTTCTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGGCCCTTAAGTCTGCTCATTTTCTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
QY 121 CGATTTCAGGGGAGTGAATCTGGGACAATTACACTCTCACCATTGAGCGCTGAGCCT 240
DB 181 AGGTTTCAGGGGAGTGAATCTGGGACAATTACACTCTCACCATTGAGCGCTGAGCCT 240
QY 241 GAAGATTTTGTACTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCCTTGGGCCAA 300
DB 241 GAAGATTTTGTCAACTTACTGTCTCAACAGAGTTTACAGTACCCCGATCCTTGGGCCAA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGAGATTAAA 321
RESULT 9
AAH47731
ID AAH47731 standard; DNA; 321 BP.
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XX AAH47731;
AC 30-NOV-2001 (first entry)
XX Nucleotide sequence of seq Id No. 74.
DE Gene library; immunoglobulin; antibody library; human; ds.
XX Homo sapiens.
XX MO200162907-A1.
XX 30-AUG-2001.
XX 22-FEB-2001; 2001WO-JP001298.
XX 22-FEB-2000; 2000JP-00050543.
XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX MPI; 2001-565420/63.
DR P-PSDB; AAG65567.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
XX Examples; p 149; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
XX Sequence 321 BP; 87 A; 87 C; 72 G; 75 T; 0 U; 0 Other;
SQ
Query Match 75.6%; Score 242.6; DB 4; Length 321;
Best Local Similarity 84.7%; Pred. No. 3.8e-68;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCTGTCTGATCTGTAGAGACAGATCAC 60
DB 1 GACATCGTATGACCCAGTCTCCATCTCCTGTCTGATCTGTAGAGACAGATCAC 60
QY 61 ATCACTTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCCGGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGAGAAACCA 120
QY 121 GGACAGCCTCTTAAGTCTGCTCATTTTCTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGGCCCTTAAGTCTGCTCATTTTCTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
QY 121 CGATTTCAGGGGAGTGAATCTGGGACAATTACACTCTCACCATTGAGCGCTGAGCCT 240
DB 181 AGGTTTCAGGGGAGTGAATCTGGGACAATTACACTCTCACCATTGAGCGCTGAGCCT 240
QY 241 GAAGATTTTGTACTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCCTTGGGCCAA 300
DB 241 GAAGATTTTGTCAACTTACTGTCTCAACAGAGTTTACAGTACCCCGATCCTTGGGCCAA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGAGATTAAA 321
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RESULT 10
AAH68651
ID AAH68651 standard; DNA; 321 BP.

XX AC AAH68651;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain I06 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UNPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

XX P-PSDB; AAG93594.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.

XX Example 2; Col 55; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (1) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 86 A; 90 C; 73 G; 72 T; 0 U; 0 Other;

Query Match 75.0%; Score 240.8; DB 5; Length 321;
Best Local Similarity 85.1%; Pred. No. 1.4e-67;
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY	6	CCAGATGACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGAGAGAGAGTCAACATC	65
DB	3	CGAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGAGAGAGAGTCAACATC	62
QY	66	TTGCCGGGCAAGTCAGAGCATTAGCAGTATTAAATTGATATCAGCAGAAACAGGACA	125
DB	63	TTGCCGGGCAAGTCAGAGCATTAGCAGTATTAAATTGATATCAGCAGAAACAGGACA	122
QY	126	GCCTCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT	185
DB	123	AGCCCTTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT	182
QY	186	CAGCGGCAAGTATCTGGGCAAAATTACATCTCAGCATTAGAGAGCTGAGCTTGAAGA	245
DB	183	CAGTGGCAGTGTGATCTGGGCAAAATTACATCTCAGCATTAGAGAGCTGAGCTTGAAGA	242
QY	246	TTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTGGGCAAGGAGC	305

DB 243 TTTTCACTTACTACTCTCAACAGAGTATAGATCCCGATCACTTGGGCAAGGAGC 302

QY 306 ACGACTGACATTCACA 321

DB 303 ACGACTGAGATTAA 318

RESULT 11

ACD45315
ID ACD45315 standard; DNA; 321 BP.

XX ACD45315;

XX 12-SEP-2003 (first entry)

XX Anti-Rh(D) chain I06 DNA.

XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UNPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2003-512273/48.

XX P-PSDB; ABO27401.

XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
PT Claim 12; Page 40; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 86 A; 90 C; 73 G; 72 T; 0 U; 0 Other;

Query Match 75.0%; Score 240.8; DB 9; Length 321;
Best Local Similarity 85.1%; Pred. No. 1.4e-67;
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY	6	CCAGATGACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGAGAGAGAGTCAACATC	65
DB	3	CGAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGAGAGAGAGTCAACATC	62
QY	66	TTGCCGGGCAAGTCAGAGCATTAGCAGTATTAAATTGATATCAGCAGAAACAGGACA	125
DB	63	TTGCCGGGCAAGTCAGAGCATTAGCAGTATTAAATTGATATCAGCAGAAACAGGACA	122
QY	126	GCCTCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT	185
DB	123	AGCCCTTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT	182
QY	186	CAGCGGCAAGTATCTGGGCAAAATTACATCTCAGCATTAGAGAGCTGAGCTTGAAGA	245
DB	183	CAGTGGCAGTGTGATCTGGGCAAAATTACATCTCAGCATTAGAGAGCTGAGCTTGAAGA	242

XX Huang H, Holmes S, Mason S;
 XX
 DR MPI; 2004-411694/38.
 DR P-PSDB; ADO36498.
 XX
 PT New human monoclonal antibody to heparanase, for use in treating or
 PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
 PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
 PT disease.
 XX
 PS Claim 8; SEQ ID NO 11; 108bp; English.
 XX
 CC The present invention describes an isolated human monoclonal antibody
 CC which binds to and inhibits activity of human heparanase. Human anti-
 CC heparanase antibodies of the present invention have cytostatic,
 CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
 CC dermatological, antidiabetic, neuroprotective and nootropic
 CC activities, and can be used as heparanase antagonists. The antibody,
 CC methods and compositions of the present invention are useful in treating
 CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
 CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
 CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
 CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
 CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
 CC and Alzheimer's disease. The present sequence encodes a human anti-
 CC heparanase 1382 VP amino acid sequence, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 321 BP; 81 A; 87 C; 76 G; 77 T; 0 U; 0 Other;
 XX
 Query Match 74.8%; Score 240.2; DB 12; Length 321;
 Best Local Similarity 84.9%; Pred. No. 2.3e-67;
 Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 5 TCCAGATGACCCAGTCCATCTCCCTGTGTCATCTGTAGAGACAGAGTCCACATCA 64
 DB 5 TCCAGTGAACCCAGTCCATCTCCCTGTGTCATCTGTAGAGACAGAGTCCACATCA 64
 QY 65 CTTCGCGGCAAGTCAGAGCATTTAGAGCTATTAAATTGGTATCAGCAAAACAGAGAC 124
 DB 65 CTTCGCGGCAAGTCAGAGCATTTAGAGCTATTAAATTGGTATCAGCAAAACAGAGAC 124
 QY 125 AGCCTCTAAGCTGCTATTACTGTGGGCACTACCCGGGAATCCGGGGTCCCTGACCGAT 184
 DB 125 AGCCTCTAAGCTGCTATTACTGTGGGCACTACCCGGGAATCCGGGGTCCCTGACCGAT 184
 QY 185 TCAGCGGAGTGAATCTGGGACAAATTATGACTCTCAGCATCAGAGCCTGACGCTGAAG 244
 DB 185 TCAGCGGAGTGAATCTGGGACAAATTATGACTCTCAGCATCAGAGCCTGACGCTGAAG 244
 QY 245 ATTTTGCTACTTACTTTGTCAACAGCTGACAGTTTGCCGATCACCTTGGCCCAAGGGA 304
 DB 245 ATTTTGCTACTTACTTTGTCAACAGCTGACAGTTTGCCGATCACCTTGGCCCAAGGGA 304
 QY 305 CACGACTGAGCATTTCAA 321
 DB 305 CACGACTGAGCATTTCAA 321
 RESULT 14
 ADD89879
 ID ADD89879 standard; cDNA; 327 BP.
 XX
 AC ADD89879;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human anti-TNF antibody 9C1A light chain variable region coding sequence.
 XX Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;
 KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
 KW neuroprotective; gene; ss.

XX OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..327
 XX FT /*tag= a
 XX FT /partial
 XX FT /product= "9C1A light chain variable region"
 XX FT /note= "No start or stop codon"
 XX
 PN WO2003083061-A2.
 XX
 PD 09-OCT-2003.
 XX
 PF 24-MAR-2003; 2003WO-US009072.
 XX
 PR 26-MAR-2002; 2002US-0367903P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Giles-Komar J, Scallon BJ, Carton JM;
 XX
 DR MPI; 2003-804040/75.
 DR P-PSDB; ADD89870.
 XX
 PT New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
 PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,
 PT anorexia, cachexia, or bacterial infection.
 XX
 PS Example 4; Fig 3A; 87bp; English.
 XX
 CC The present sequence is the coding sequence of the light chain variable
 CC region of human anti-tumour necrosis factor (TNF) monoclonal antibody
 CC 9C1A. This human TNF reactive IgG monoclonal antibody was generated by
 CC cloning variable and constant region DNA in vector pC4 and expression in
 CC CHO cells. The invention provides isolated human, primate, rodent,
 CC mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies,
 CC immunoglobulins, their cleavage products, other specified portions and
 CC variants, as well as anti-TNF antibody compositions, nucleic acids
 CC encoding these, vectors, host cells, methods for producing the antibodies
 CC using a host cell, transgenic animal or transgenic plant or plant cell,
 CC and therapeutic compositions, methods and devices. The antibody, nucleic
 CC acid, protein, composition and methods are useful for diagnosing or
 CC treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia,
 CC or an immune, cardiovascular, infectious, and/or neurological disease.
 XX
 SQ Sequence 327 BP; 84 A; 89 C; 76 G; 78 T; 0 U; 0 Other;
 XX
 Query Match 74.3%; Score 238.6; DB 10; Length 327;
 Best Local Similarity 84.5%; Pred. No. 7.5e-67;
 Matches 268; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 5 TCCAGATGACCCAGTCCATCTCCCTGTGTCATCTGTAGAGACAGAGTCCACATCA 64
 DB 5 TCCAGTGAACCCAGTCCATCTCCCTGTGTCATCTGTAGAGACAGAGTCCACATCA 64
 QY 65 CTTCGCGGCAAGTCAGAGCATTTAGAGCTATTAAATTGGTATCAGCAAAACAGAGAC 124
 DB 65 CTTCGCGGCAAGTCAGAGCATTTAGAGCTATTAAATTGGTATCAGCAAAACAGAGAC 124
 QY 125 AGCCTCTAAGCTGCTATTACTGTGGGCACTACCCGGGAATCCGGGGTCCCTGACCGAT 184
 DB 125 AGCCTCTAAGCTGCTATTACTGTGGGCACTACCCGGGAATCCGGGGTCCCTGACCGAT 184
 QY 185 TCAGCGGAGTGAATCTGGGACAAATTATGACTCTCAGCATCAGAGCCTGACGCTGAAG 244
 DB 185 TCAGCGGAGTGAATCTGGGACAAATTATGACTCTCAGCATCAGAGCCTGACGCTGAAG 244
 QY 245 ATTTTGCTACTTACTTTGTCAACAGCTGACAGTTTGCCGATCACCTTGGCCCAAGGGA 304
 DB 245 ATTTTGCTACTTACTTTGTCAACAGCTGACAGTTTGCCGATCACCTTGGCCCAAGGGA 304
 QY 305 CACGACTGAGCATTTCAA 321

Db 305 CACGACTGGAGATTAA 321

RESULT 15

AD564656
ID AD564656 strand; DNA; 327 BP.

AC AD564656;

DT 16-DEC-2004 (first entry)

DE Human 9C11C light chain protein encoding DNA.

XX Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
XX obesity; immune related disease; rheumatoid arthritis;
XX cardiovascular disease; stroke; malignant disease; leukaemia;
XX neurological disease; multiple sclerosis; infection; hepatitis;
XX anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
XX neuroprotective; antibacterial; antiinflammatory; hepatotropic; vitruclide;
XX human; 9C11C; light chain; gene; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 10..327

XX FT /*tag= a

XX FT /partial

XX FT /note= "No start and stop codon"

XX FT /product= "9C11C light chain protein"

XX US2004185047-A1.

XX 23-SEP-2004.

XX 21-MAR-2003; 2003US-00394471.

XX 21-MAR-2003; 2003US-00394471.

XX (GILE/) GILES-KOMAR J.

XX (SCAL/) SCALON B J.

XX (CART/) CARTON J M.

XX Giles-Komar J, Scallon BJ, Carton JM;

XX MPI: 2004-676151/66.

XX P-PSDB; AD564657.

XX Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody

XX capable of inhibiting binding of TNF alpha to TNF receptor, useful for

XX treating TNF-related diseases such as obesity or rheumatoid arthritis.

XX Example 4; Fig 3; 45pp; English.

XX The present invention relates to a mammalian anti-tumour necrosis factor

XX (TNF) antibody capable of inhibiting binding of TNF alpha to TNF

XX receptor. The invention is useful for diagnosing or treating an anti-TNF

XX related condition in a cell, tissue, organ or animal and in

XX immunotherapy. The invention is also useful for treating TNF related

XX diseases chosen from obesity, immune related disease such as rheumatoid

XX arthritis, cardiovascular disease such as stroke, malignant disease such

XX as leukemia, neurological disease such as multiple sclerosis and

XX bacterial or viral infections such as hepatitis. The present sequence is

XX the human 9C11C light chain protein (variable region and J-region)

XX encoding DNA. This sequence is used in the exemplification of the

XX invention.

XX Sequence 327 BP; 84 A; 89 C; 76 G; 78 T; 0 U; 0 Other;

XX Query Match 74.3%; Score 238.6; DB 13; Length 327;

XX Best Local Similarity 84.5%; Pred. No. 7.5e-67;

XX Matches 268; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 5 TCAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGACTCAACATCA 64
Db 5 TCAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGACTCAACATCA 64
QY 65 CTGGCCGGGCAAGTCAGAGCATTTGACAGCTATTTAAATTGGTATCAGCAAAACCAAGAC 124
Db 65 CTGGCCGGGCAAGTCAGAGCATTTGACAGCTATTTAGCCTGTATCAGCAAAACCAAGAC 124
QY 125 AGCCTCCTAAGCTGCTCATTTACTGGGCACTACCCGGGATCCGCTGACCGAT 184
Db 125 AAGCTCTAAGCTGCTCATTTACTGGGCACTACCCGGGATCCGCTGACCGAT 184
QY 185 TCAGGCGAGTGAATCTGGGCAAAATTACCTTCACCATCAGAGCCTGACGCTGAG 244
Db 185 TCAGGCGAGTGAATCTGGGCAAAATTACCTTCACCATCAGAGCCTGACGCTGAG 244
QY 245 ATTTTGCTACTTACTTTTGTCAACAGTGTGACAGTTGGCGATCACTTGGCCCAAGGA 304
Db 245 ATTTTGCTACTTACTTTTGTCAACAGTGTGACAGTTAAAGTTAACCGATCACTTGGCCCAAGGA 304
QY 305 CACGACTGGAGATTCAA 321
Db 305 CACGACTGGAGATTCAA 321

Search completed: September 11, 2005, 20:26:01
Job time : 341.536 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 18:08:48 ; Search time 2579.67 Seconds
(without alignments)
4736.504 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 gagccacagatgacccacgctc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic1:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsel1:*
9: gb_gsel2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238.4	74.3	353	2	AM404894 UI-HF-BL0
2	237.8	74.1	794	6	CB955875 AGENCOURT
3	236.2	73.6	621	4	BM171889 ImageQC_3
4	236.2	73.6	748	6	CB957070 AGENCOURT
5	234.6	73.1	826	6	BG742662 602633264
6	233	72.6	709	6	CD690167 EST6690 h
7	233	72.6	781	6	CB985512 AGENCOURT
8	231.6	72.1	553	6	CD705041 EST21568
9	231.4	72.1	421	2	AM406227 UI-HF-BL0
10	231.4	72.1	422	2	AM407904 UI-HF-BL0
11	231.4	72.1	521	6	CD707755 EST24282
12	231.4	72.1	587	6	BG756289 602713607
13	231.4	72.1	624	6	CD690145 EST6668 h
14	230.6	71.8	570	4	BG536784 602366318
15	229.8	71.6	486	6	CD683960 EST480 hu
16	229.8	71.6	493	2	AM405753 UI-HF-BL0
17	229.8	71.6	797	6	CB987347 AGENCOURT
18	229.8	71.6	831	6	CB987031 AGENCOURT
19	228.2	71.1	525	6	CD705928 EST24455
20	228.2	71.1	708	6	CB956923 AGENCOURT
21	228.2	71.1	773	4	BM007845 603617528
22	227.4	70.8	339	4	AB107216 AB107216
23	227.4	70.8	499	6	CD685478 EST1998 h
24	226.6	70.6	487	2	AM405301 UI-HF-BL0

25	226.6	70.6	559	4	BG547768 602575646
26	226.6	70.6	693	6	CD684441 EST961 hu
27	226.6	70.6	754	6	CB986767 AGENCOURT
28	226.6	70.6	785	6	CB955817 AGENCOURT
29	226.6	70.6	864	4	BG548281 602575248
30	226.6	70.6	923	5	BQ882857 AGENCOURT
31	226.4	70.5	740	6	CB987627 AGENCOURT
32	226.4	70.5	756	6	CB984720 AGENCOURT
33	225.8	70.3	608	2	AM404714 UI-HF-BL0
34	225.8	70.3	921	4	BG341239 602463904
35	225	70.1	460	2	AM404992 UI-HF-BL0
36	225	70.1	510	6	AM405906 UI-HF-BL0
37	225	70.1	550	6	CD694557 EST11080
38	225	70.1	550	6	CD709957 EST26484
39	225	70.1	566	2	AM406081 UI-HF-BL0
40	225	70.1	695	6	CD683876 EST396 hu
41	225	70.1	724	6	CB959008 AGENCOURT
42	225	70.1	742	6	CB984723 AGENCOURT
43	225	70.1	759	6	CB986444 AGENCOURT
44	225	70.1	785	6	CB986976 AGENCOURT
45	225	70.1	820	6	CB956240 AGENCOURT

ALIGNMENTS

RESULT 1
AM404894
LOCUS
DEFINITION
UI-HF-BL0-acn-f-07-0-UI.x1 NIH MGC_37 Homo sapiens CDNA clone
IMAGE:3059844 5', mRNA sequence.
AM404894
ACCESSION
AM404894.1 GI:6923951
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgs.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www.bio.lnl.gov/bbtp/image/image.html
Seq primer: M13 Forward.

FEATURES

source
1..353
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059844"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC_37"
/note="Vector: pRT3-Pac; Site 1: NotI; Site 2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match
Best Local Similarity
74.3%; Score 238.4; DB 2; Length 353;
85.3%; Pred. No. 5.8e+66;

Matches 266; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCCATCCCTGCTGCACTGTGAGAGACAGAGTCAACC 60
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 DB 42 GACATCCAGATGACCCAGTCCATCCCTGCTGCACTGTGAGAGACAGAGTCAACC 101
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 QY 61 ATCACTTCCGCGGCAAGTCAGAGCATTAACAGCTATTAAATGGATACAGAAACCA 120
 |||
 DB 102 ATCACTTCCGCGGCAAGTCAGAGCATTAACAGCTATTAAATGGATACAGAAACCA 161
 |||
 QY 121 GGAACGCTCTTACGTCTCATTTACTGGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
 |||
 DB 162 GGGAAAGCCCTTACGCTCTGATCTATGCTGATCCAGATTTGCAAGAGTGGGGTCCCATCA 221
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 QY 181 CGATTACAGGGGAGATCTGGGACAAATTAACATCTGACCATCAAGCCTGAGAGCT 240
 |||
 DB 222 AGGTCAGTGGCAGATGATGGGACAGATTTCACTTCACATTCAGAGTCTGCAACT 281
 |||
 QY 241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACTTGGCCCA 300
 |||
 DB 282 GAAGATTTTGCAACTTACTTACTGTCACAGAGTTACAGTTTCCGCACTTCCGCCAA 341
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 QY 301 GGGACACGACTG 312
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 DB 342 GGGACACGACTG 353
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RESULT 2
 LOCUS CB955875 794 bp mRNA linear EST 29-APR-2003
 DEFINITION AGENCOURT 13779371 NIH MGC_184 Homo sapiens cDNA clone
 IMAGE:30349554 5', mRNA sequence.

ACCESSION CB955875
 VERSION CB955875.1 GI:30211993
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 794) Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgsabers@mail.nih.gov

REFERENCE CDNA Library Preparation: Clontech Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

COMMENT Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

FEATURES
 source Plate: NDCM144 row: a column: 19
 High quality sequence stop: 520.
 Location/Qualifiers

1. 794
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30349554"
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 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: sfli (ggccattagggc); Site_2: sfli (ggcgcctgggc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATTAAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones

ORIGIN
 and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 74.1%; Score 237.8; DB 6; Length 794;
 Best Local Similarity 83.8%; Pred. No. 1.2e-65;
 Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCCATCCCTGCTGCACTGTGAGAGACAGAGTCAACC 60
 |||
 DB 94 GACATCCAGATGACCCAGTCCATCCCTGCTGCACTGTGAGAGACAGAGTCAACC 153
 |||
 QY 61 ATCACTTCCGCGGCAAGTCAGAGCATTAACAGCTATTAAATGGATACAGAAACCA 120
 |||
 DB 154 ATCACTTCCGCGGCAAGTCAGAGCATTAACAGCTATTAAATGGATACAGAAACCA 213
 |||
 QY 121 GGAACGCTCTTACGTCTCATTTACTGGCATCTACCCGGGAATCCGGGCTCCCTGAC 180
 |||
 DB 214 GGGAAAGCCCTTACGCTCTGATCTATGCTGATCCAGATTTGCAAGAGTGGGGTCCCATCA 273
 |||
 QY 181 CGATTACAGGGGAGATCTGGGACAAATTAACATCTGACCATCAAGCCTGAGAGCT 240
 |||
 DB 274 AGGTCAGTGGCAGATGATGGGACAGATTTCACTTCACATTCAGAGTCTGCAACT 333
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 QY 241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACTTGGCCCA 300
 |||
 DB 334 GAAGATTTTGCAACTTACTTACTGTCACAGAGTTACAGTTTCCGCACTTCCGCCAA 393
 |||
 QY 301 GGGACACGACTGAGCATTTCA 321
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 DB 394 GGGACACGACTGAGCATTTAA 414
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RESULT 3
 LOCUS BM171889 621 bp mRNA linear EST 04-DEC-2001
 DEFINITION imagegc_3_2001/smm27bdf41.x1 NIH_MGC_77 Homo sapiens cDNA clone
 IMAGE:4690877 5', mRNA sequence.

ACCESSION BM171889
 VERSION BM171889.1 GI:17311452
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 621) Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (2001)
 JOURNAL Contact: Prange CK

COMMENT The I.M.A.G.E. Consortium quality control effort: clone
 resequencing for verification
 Other ESTs: BG536784

FEATURES
 source Plate: Prange CK
 High quality sequence stop: 621.
 Location/Qualifiers

1. 621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: sfli (ggccattagggc); Site_2: sfli (ggcgcctgggc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATTAAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones

This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact

inf@image.llnl.gov.
 Plate: LDCM1509 row: c column: 6
 Seq primer: -21ml3
 High quality sequence stop: 621.
 Location/Qualifiers

1. 621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"


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/clone="IMAGE:4690877"  
/lab_host="DH10B (T1 phage-resistant)"  
/clone_lib="NIH_MGC_77"  
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:  
Site1 (ggccgctcggcc); Site_2: Site1 (ggccatcggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCATTATGAGC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGCCGACG-dt(10)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH_MGC Library."
```

ORIGIN

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Query Match 73.6%; Score 236.2; DB 4; Length 621;  
Best Local Similarity 83.5%; Pred. No. 3,7e-65;  
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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ORIGIN

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Query Match 73.6%; Score 236.2; DB 6; Length 748;  
Best Local Similarity 83.5%; Pred. No. 4e-65;  
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:30350034"  
/lab_host="DH10B (T1 phage-resistant)"  
/clone_lib="NIH_MGC_184"  
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:  
Site1 (ggccatcggcc); Site_2: Site1 (ggccgctcggcc);  
Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCATTATGAGC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGGCGCCGACG-dt(10)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH_MGC Library."
```

```
1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGATCACC 60  
|||  
90 GATTGCGAATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGATCACC 149  
61 ATCACTTGGCCGGCAAGTACAGACATTAGACGCTATTAAATTGGTATCAGAGAAACCA 120  
150 GCCACTTGGCCGGCAAGTACAGACATTAAACAATATTAAATTGGTATCAGAGAAACCA 209  
121 GGAACAGCTCTTAACTGCTCATTACTGGGCACTTACCCGGGAATCCGGGCTCCTGAC 180  
210 GGGCAAGCCCTTAAAGTCTGATTTATGGTGCATCCATTTGGCAAGTGGGGTCCCATCA 269  
181 CGATTAGAGGGAGGATCTGGGACAAATTACATCTCAACCATCAGACGCGCGAGCCT 240  
270 AGGTTAGTGGGAGTGTGAGATCTGGGACAGATTCTCACTCAACATCAGAGTCTGCAACCT 329  
241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGATTGGCCGATCCTTGGCCAA 300  
330 GAAAGATTTTGGCACTTACTACTCTCAACAGACTTTTATTCCTGATCCTTGGCCAA 389  
301 GGGACACGACTGGACATTCAA 321  
390 GGGACACGACTGGAGATTAA 410
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RESULT 4  
LOCUS CB957070 748 bp mRNA linear EST 29-APR-2003  
DEFINITION AGENCOURT 13777897 NIH_MGC_184 Homo sapiens cDNA clone  
IMAGE:30350034 5', mRNA sequence.  
CB957070  
VERSION CB957070.1 GI:30213187  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 748)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLOUTech Laboratories, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDCM145 row: e column: 19  
High quality sequence stop: 507.  
Location/Qualifiers  
1. 748
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FEATURES

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source
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1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGATCACC 60  
|||  
89 GATTCGAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGATCACC 148  
61 ATCACTTGGCCGGCAAGTACAGACATTAGACGCTATTAAATTGGTATCAGAGAAACCA 120  
149 ATCACTTGGCCGGCAAGTACAGACATTACAGTTTAAATTGGTATCAGAGAAACCA 208  
121 GGAACAGCTCTTAACTGCTCATTACTGGGCACTTACCCGGGAATCCGGGCTCCTGAC 180  
209 GGGAAACCCCTTAAAGTCTGATTTATGGTGCATCCATTTGGCAAGTGGGGTCCCATCA 268  
181 CGATTAGAGGGAGGATCTGGGACAAATTACATCTCAACCATCAGACGCGCGAGCCT 240  
269 AGTTCAGTGGGAGTGTGAGATCTGGGACAGATTCTCACTCAACATCAGAGTCTGCAACCT 328  
241 GAAGATTTTGTACTTACTTTTGTCAACAGTCTGACAGATTGGCCGATCCTTGGCCAA 300  
329 GATGATTTTGGCACTTACTCTCTCAACAGATTACATTCATCCCGATCCTTGGCCAA 388  
301 GGGACACGACTGGACATTCAA 321  
389 GGGACACGACTGGAGATTAA 409
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RESULT 5  
LOCUS BG742662 826 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602633264F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:478726 5',  
mRNA sequence.  
BG742662  
VERSION BG742662.1 GI:14053315  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 826)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be
```

```
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT
```

Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10634 row: 0 Column: 15
High quality sequence stop: 824.
Location/Qualifiers

FEATURES

source

1..826

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4778726"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NciI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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ORIGIN

Query Match 73.1%; Score 234.6; DB 4; Length 826;
Best Local Similarity 83.2%; Pred. No. 1.4e-64;

Matches 267; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTCTGTCTGCACTCTGTGAGAGACGAGTCACC 60
DB 55 GACATCCAGATGACCCAGTCTCCATCTCTCTGTCTGCACTCTGTGAGAGACGAGTCACC 114
QY 61 ATCACTTCCCGGCGAGTCAGACGATTAAGTATGATCAGAGAAACA 120
DB 115 ATCACTTCCCGGCGAGTCAGACGATTAAGTATGATCAGAGAAACA 174
QY 121 GGACAGCCTCTAAGCTGCTCATTTACTGCGCATCTACCCGGGAAATCCGGGCTCCCTGAC 180
DB 175 GGGAAAGCCCTTAAGCTGCTCATTTACTGCGCATCTACCCGGGAAATCCGGGCTCCCTGAC 234
QY 181 CGATTACAGCGGAGTGAATCTGGGACAAATTACACTCTCAGCAGCCTGACGCT 240
DB 235 AGGTTCAAGTGGAGTGGATCTGGGACAGATTTCACCTCAGCATCAGTATGTCGAAACCT 294
QY 241 GAAGATTTTGCTACTTCTTTGTCAACAGTCTGACAGTTTCCGATCCGATCCGACCA 300
DB 295 GAAGATTTTGCTACTTCTTTGTCAACAGTCTGACAGTTTCCGATCCGATCCGACCA 354
QY 301 GGGACACGACTGAGCATTTCA 321
DB 355 GGGACACGACTGAGCATTTAA 375
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RESULT 6
CD690167 709 bp mRNA linear EST 25-JUN-2003
LOCUS CD690167
DEFINITION EST6690 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690167
VERSION CD690167.1 GI:32210659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 709)
AUTHORS Liu,X.-O., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES

source

1..709

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/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
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ORIGIN

Query Match 72.6%; Score 233; DB 6; Length 709;
Best Local Similarity 82.9%; Pred. No. 4.2e-64;

Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTCTGTCTGCACTCTGTGAGAGACGATCAC 60
DB 123 GACATCCAGATGACCCAGTCTCCATCTCTCTGTCTGCACTCTGTGAGAGACGATCAC 182
QY 61 ATCACTTCCCGGCGAGTCAGACGATTAAGTATGATCAGAGAAACA 120
DB 183 ATCACTTCCCGGCGAGTCAGACGATTAAGTATGATCAGAGAAACA 242
QY 121 GGACAGCCTCTAAGCTGCTCATTTACTGCGCATCTACCCGGGAAATCCGGGCTCCCTGAC 180
DB 243 GGGAAAGCCCTTAAGCTGCTCATTTACTGCGCATCTACCCGGGAAATCCGGGCTCCCTGAC 302
QY 181 CGATTACAGCGGAGTGAATCTGGGACAAATTACACTCTCAGCAGCCTGACGCT 240
DB 303 AGGTTCAAGTGGAGTGGATCTGGGACAGATTTCACCTCAGCATCAGCAGCCTGACGCT 362
QY 241 GAAGATTTTGCTACTTCTTTGTCAACAGTCTGACAGTTTCCGATCCGATCCGACCA 300
DB 363 GAAGATTTTGCTACTTCTTTGTCAACAGTCTGACAGTTTCCGATCCGATCCGACCA 422
QY 301 GGGACACGACTGAGCATTTCA 321
DB 423 GGGACACGACTGAGCATTTAA 443
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RESULT 7
CB985512 781 bp mRNA linear EST 01-MAY-2003
LOCUS CB985512
DEFINITION IMAGE30327573 5', mRNA sequence.
ACCESSION CB985512
VERSION CB985512.1 GI:30280036
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 781)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokvics
cDNA Library Preparation: CLOUTCH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM136 row: m column: 22
High quality sequence stop: 390.
Location/Qualifiers

FEATURES

source

1..781

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30327573"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
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sfll (ggccatcatg9cc); Site 2: sfll (ggccctctg9cc);
Library is oligo-dt primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:
5'-ATCTAGAGCGCCGCGCGCAGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 72.6%; Score 233; DB 6; Length 781;
Best Local Similarity 82.9%; Pred. No. 4,4e-64;
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATGAGAGACAGATCACC 60
DB 89 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATGAGAGACAGATCACC 148
QY 61 ATCACTTGGCGGCAAGTCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 120
DB 149 ATCACTTGGCGGCAAGTCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 208
QY 121 GAGACGCTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180
DB 209 GGGAAAGCCCTTAATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 268
QY 181 CGATTCAGCGGCGAGTGAATCTGAGCAATTAACCTGACATGACAGCTGACAGCT 240
DB 269 AGGTCAGTGGCAGTGAATCTGAGCAATTAACCTGACATGACAGCTGACAGCT 328
QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTCTGACAGTTGCGGATCACCCTTGGCCAA 300
DB 329 GAAGATTTTGTCTACTTCTTGTCAACAGTCTGACAGTTGCGGATCACCCTTGGCCAA 368
QY 301 GGGACACGACTGACATTCMA 321
DB 389 GGGACACGACTGACATTCMA 409

RESULT 8
CD705041 553 bp mRNA linear EST 25-JUN-2003
LOCUS CD705041 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION CD705041
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Liu X.-O., Zhou Y., Zhang L.-J., Xu H., Chen H.-K., Pan Z.-G. and
Zeng Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn.
Location/Qualifiers
1. 553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.6; DB 6; Length 553;
Best Local Similarity 83.0%; Pred. No. 1.1e-63;
Matches 264; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTGATGAGAGACAGATCACC 60
DB 123 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATGAGAGACAGATCACC 182
QY 61 ATCACTTGGCGGCAAGTCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 120
DB 183 ATCACTTGGCGGCAAGTCAAGATGAGATGAGATGAGATGAGATGAGATGAGAT 242
QY 121 GAGACGCTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 180
DB 243 GGGAAAGCCCTTAATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAA 302
QY 181 CGATTCAGCGGCGAGTGAATCTGAGCAATTAACCTGACATGACAGCTGACAGCT 240
DB 303 AGGTCAGTGGCAGTGAATCTGAGCAATTAACCTGACATGACAGCTGACAGCT 362
QY 241 GAAGATTTTGTCTACTTCTTGTCAACAGTCTGACAGTTGCGGATCACCCTTGGCCAA 300
DB 363 GAAGATTTTGTCTACTTCTTGTCAACAGTCTGACAGTTGCGGATCACCCTTGGCCAA 422
QY 301 GGGACACGACTGACATTCMA 318
DB 423 GGGACACGACTGACATTCMA 440

RESULT 9
AM406227 421 bp mRNA linear EST 16-FEB-2000
LOCUS AM406227
DEFINITION
ACCESSION AM406227
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaab@rs-mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1. 421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059726"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA"

ORIGIN

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 72.1%; Score 231.4; DB 2; Length 421;

Best Local Similarity 82.6%; Pred. No. 1.2e-63;

Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAAC 60
DB 10 GACATTCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAAC 69
QY 61 ATCACTTCGCGGAGAGTCAAGAGATTAAGATTAATTTGATGAGAGAAACA 120
DB 70 ATCACTTCGCGGAGAGTCAAGAGTTCGAGAGTGTATGCTGTATGAGAGAAACA 129
QY 121 GGACAGCCTCTTAAGCTCTCATTTACTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
DB 130 GGACATGCCCTTAAGCTCTCATTTACTGGGCAATCAACCGGGAATCCGGGTCCTGAC 189
QY 181 CGATTACAGGAGAGTGAATCTGGGCAATTAACATCTGACATGACAGCCTGACGCT 240
DB 190 AGGTTACAGGAGAGTGAATCTGGGCAATTAACATCTGACATGACAGCCTGACGCT 249
QY 241 GAAGATTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACTTCGGCCAA 300
DB 250 GAAGATTTGTACTTACTTATTTGTCAACAGGCTTAACACTTCCGATCACTTCGGCCAA 309
QY 301 GGGACACGACTGGACATTTCAA 321
DB 310 GGGACACGACTGGACATTTCAA 330

RESULT 10

AM407904

LOCUS 422 bp mRNA linear EST 16-FEB-2000

DEFINITION UI-HF-BL0-add-a-01-0-UI.r2 NIH MGC_37 Homo sapiens cDNA clone

IMAGE:3061128 5', mRNA sequence.

ACCESSION AM407904

VERSION AM407904.1 GI:6926961

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 422)

NIH-MGC http://mgi.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

www-bio.lnl.gov/dbp/image/image.html

Seq primer: M3 Forward.

Location/Qualifiers

1..422

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3061128"

/issue_type="lymph"

/cell_type="germinal center B cells"

/lab_host="DH10B (LTI)"

/clone_lib="NIH_MGC_37"

/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;

ORIGIN

Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 72.1%; Score 231.4; DB 2; Length 422;

Best Local Similarity 82.6%; Pred. No. 1.2e-63;

Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAAC 60
DB 23 GACATTCAGATGACCCAGTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAAC 82
QY 61 ATCACTTCGCGGAGAGTCAAGAGATTAAGATTAATTTGATGAGAGAAACA 120
DB 83 ATCACTTCGCGGAGAGTCAAGAGATTAAGATTAATTTGATGAGAGAAACA 142
QY 121 GGACAGCCTCTTAAGCTCTCATTTACTGGGCAATCAACCGGGAATCCGGGTCCTGAC 180
DB 143 GGGAAGCCCTTAAGCTCTCATTTACTGGGCAATCAACCGGGAATCCGGGTCCTGAC 202
QY 181 CGATTACAGGAGAGTGAATCTGGGCAATTAACATCTGACATGACAGCCTGACGCT 240
DB 203 AGGTTACAGGAGAGTGAATCTGGGCAATTAACATCTGACATGACAGCCTGACGCT 262
QY 241 GAAGATTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACTTCGGCCAA 300
DB 263 GAAGATTTGTACTTACTTATTTGTCAACAGGCTTAACACTTCCGATCACTTCGGCCAA 322
QY 301 GGGACACGACTGGACATTTCAA 321
DB 323 GGGACACGACTGGACATTTCAA 343

RESULT 11

CD707755

LOCUS 521 bp mRNA linear EST 25-JUN-2003

DEFINITION EST24282 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD707755

VERSION CD707755.1 GI:32238385

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 521)

Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and

Zeng,Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

Contact: Yixin zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn

Location/Qualifiers

1..521

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/issue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA

library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.4; DB 6; Length 521;

Best Local Similarity 82.6%; Pred. No. 1.3e-63;

Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
|||
Db 91 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 150
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGAGTATTTAAATTGGTATCAGAGAAACA 120
151 ATCACTTGGCCAGGCGAGTCAAGACATTTAACTATTAAATTGGTATCAGAGAAACA 210
QY 121 GGAACAGCTCTTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
Db 211 GGGAAAGCCCTTAAGCTCTGATCTTACAGATGATCCATTTTGGAAACAGGGGTCATCA 270
QY 181 CGATTCAAGCGGCGAGTGAATCTGGGACAAATTACACTCTCAGATCAGAGCTGACGCT 240
Db 271 AGGTTCAAGTGGAGTGAATCTGGGACAGATTTTACTTCCATCAGTACAGAGCTGACGCT 330
QY 241 GAAATTTTGGCTAATTCTTTGTCAAAGTCTGACAGTTGGCGATCAGCTTGGGCA 300
Db 331 GAAGATATTGCAACATTTACTGTCAACAGTTGATTAATCTCCGATCAGCTTGGGCA 390
QY 301 GGGACAGACTGACATTCAA 321
Db 391 GGGACAGACTGAGATTAA 411

RESULT 12
LOCUS BG756289 587 bp mRNA linear EST 15-MAY-2001
DEFINITION 602713607F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853953 5',
mRNA sequence.
ACCESSION BG756289
VERSION BG756289.1 GI:14066942
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 587)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LINC1700 row: n column: 02
High quality sequence stop: 586.
Location/Qualifiers
1. 587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853953"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1; XhoI;
Site: 2; EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGAACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH-MGC Library."

ORIGIN
Query Match 72.1%; Score 231.4; DB 4; Length 587;

Best Local Similarity 82.6%; Pred. No. 1.3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
|||
Db 77 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 136
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGAGTATTTAAATTGGTATCAGAGAAACA 120
137 ATCACTTGGCCAGGCGAGTCAAGATTTAGTACTATTAAATTGGTATCAGAGAAACA 196
QY 121 GGAACAGCTCTTAAGCTGCTCATTTTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
Db 197 GGGAAAGCCCTTAAGCTCTGATCTTACAGATGATCCATTTTGGAAATAGGGTCCATCA 256
QY 181 CGATTCAAGCGGCGAGTGAATCTGGGACAAATTACACTCTCAGATCAGAGCTGACGCT 240
Db 257 AGGTTCAAGTGGGCGTGGAGTCTGGGACAGATTTTACTTCCATCAGATCAGAGCTGACGCT 316
QY 241 GAAATTTTGGCTAATTCTTTGTCAAAGTCTGACAGTTGGCGATCAGCTTGGGCA 300
Db 317 GAAGATATTGCAACATTTACTGTCAACGGCAGTGAATGCTCCGATCAGCTTGGGCA 376
QY 301 GGGACAGACTGACATTCAA 321
Db 377 GGGACAGACTGGAATTAA 397

RESULT 13
LOCUS CD690145 624 bp mRNA linear EST 25-JUN-2003
DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690145
VERSION CD690145.1 GI:32210615
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 624)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510660, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@yzu.edu.cn
Location/Qualifiers
1. 624
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 72.1%; Score 231.4; DB 6; Length 624;
Best Local Similarity 82.6%; Pred. No. 1.3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 GAGCTCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 60
|||
Db 114 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTACC 173
QY 61 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGAGTATTTAAATTGGTATCAGAGAAACA 120
174 ATCACTTGGCCGGGCAAGTCAAGACATTTAGAGAGTATTTAAATTGGTATCAGAGAAACA 233

QY	121	GGACAGCCTCCTTAAGCTGCTCA	TTTACTTACGTGGGATCTTACC	CGGAAATCCGGGGTCCCTGAC	180
DB	234	GGGAAGCCCCCTTAAGCTCCTG <td>ATCTATGCTGCATCAGTTTGGCA <td>AGTGGGGTCCCATCA</td> <td>293</td> </td>	ATCTATGCTGCATCAGTTTGGCA <td>AGTGGGGTCCCATCA</td> <td>293</td>	AGTGGGGTCCCATCA	293
QY	181	CGATTACAGCGCAGTAATCTGG <td>GCACAAATTACCTTCACCATCAG</td> <td>CGCCTGAGCCT</td> <td>240</td>	GCACAAATTACCTTCACCATCAG	CGCCTGAGCCT	240
DB	294	AGATTCAATGGCAGTGGATCTG <td>GGGACAGATTTCACTCTCCATCA</td> <td>TGACAGTCTGCAACT</td> <td>353</td>	GGGACAGATTTCACTCTCCATCA	TGACAGTCTGCAACT	353
QY	241	GAAGATTTTGTACTTACTTTTGT <td>CAACAGTCTGACAGTTTGGCGAT</td> <td>CACTTCGGCCAA</td> <td>300</td>	CAACAGTCTGACAGTTTGGCGAT	CACTTCGGCCAA	300
DB	354	GAAGATTTTGCACCTTACTACTG	TCAACAGAGTTACATCCCTAGA	AACTTTTGGCAG	413
QY	301	GGGACAGCAGCTGGACATTCAA		321	
DB	414	GGGACCAAGCTGGAGATCAAA		434	

RESULT 14	
BG536784	
LOCUS	BG536784
DEFINITION	BG536784 570 bp mRNA linear EST 03-APR-2001
	60256618r1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4690877 5' _
	mRNA sequence.

ACCESSION	BG536784	GI:13528330
VERSION	BG536784.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
1 (bases 1 to 570)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS	NIH-MGC http://mgc.ncbi.nlm.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LITCM1509 row: c column: 06
High quality sequence stop: 568.

FEATURES	Location/Qualifiers
source	1..570

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4690877"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
5'f1 (ggcgccctcgcc); Site_2: 5'f1 (ggccattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGAGCGCGCGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 clones contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."

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Query Match	71.8%;	Score 230.6;	DB 4;	Length 570;
Best Local Similarity	84.4%;	Pred. No. 2.4e-63;		
Matches 271; Conservative	0;	Mismatches 49;	Indels 1;	Gaps 1;

Oy 1 GAGCTTCAGATGACCCAGTCTCCATCTCTCCCTGTGCATCTTAGAGACAGAGTTACC 60
 |||||
Db 91 GACATTCAGATGCCAGTCTCCATCTCTCCTTTCAATCTTGAGAGACAAGTACC 150
 |||||

QY	6	ATACATTGGCCGGGCAAGTCAGAGATTATGAGCTATTTAAATTGGTATCGAGAAACCA	120
Db	151	GTCACTTGGCCGGGCAAGTCAGAAACTTAAACAATTTTAAATTGGTATCACAAAAACCA	210
QY	121	GGAACAAGCTCTTAAGTGTCTCAATTTACTGGGATCTACCCGGGAATCCGGGGTCCCTGAC	180
Db	211	GGCAAGCC-CTTAAGTCTCTGAATTTATGGTGCATCACTTTGGCAAAATGGGGGTCCCATCA	269
QY	181	CGATTACAGGGGCAAGTCAATCTGGGCAAAATTACAATCTCAACATCAAGACGCTGCAGCCT	240
Db	270	AGGTTAGTGGCAAGTGAATCTGGAGAAAGATTTCATCTCAACATCAAGAGTCTGCACCT	329
QY	241	GAGATTTTGTCTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACCTTGGCCAA	300
Db	330	GAGATTTTGTCTACTTACTTGTCAACAGACTTTCATTATCCGATCACTTGGCCAA	389
QY	301	GGGACAGCACTGCACATTCAA	321
Db	390	GGGACAGCACTGCAGATTAAA	410

RESULT 15			
CD683960			
LOCUS	486 bp	mRNA	linear
DEFINITION	EST1480 human nasopharynx Homo sapiens cDNA, mRNA sequence.		EST 25-JUN-2003

ACCESSION	CD683960
VERSION	CD683960.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 486)	Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.	Transcriptional Gene Expression Profile of Human Nasopharynx	Unpublished (2003)	Contact: Yixin Zeng

Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsunm.edu.cn.

FEATURES	Location/Qualifiers
source	1. .486

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/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/ribose_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

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ORIGIN	Query Match
71.6%;	Score 229.8; DB 6; Length 486;

Best Local Similarity 82.2%; Pred. No. 4e-63;
Matches 264; Conservative 0; Mismatches 57; Indels 0;
Gaps 0;
1 GAGCTCCAGATGACCCAGCTTCCATCTCCCTCTGTCATCTGTTGGAGACAGATACC 60

QY	Db
61 ATCATCTTGGCCGGGAGTCAGAGCATTTTGGACGCTATTTAAATTTGGTATTCAGCAAGAAACCA 120	134 GACATCCAGATGACCCAGATTTCCATCTTCGGTGTGTCATCTGTAGAGGACAGAGTACC 153
194 ATCATCTTGGCCGGGAGTCAGAGCATTTTGGACGCTATTTAAATTTGGTATTCAGCAAGAAACCA 253	

Qy	121	GGAAGCCTCTAAGTGCATTTACTGGGCACTCCGGAGTCGGGGTCCGTAC	180
Db	254	GGAAAGCCCCTAAGTCTGATCTATGCTGCATCCAATTACAAGTGGGGTCCCATCA	313

181 CGATTACGGCAGTAATCTGGGACAAATTACACTCTACCATCAGACGCTGACGCT 240

Db	314	AGGTCAGCGCAGTGATCTGGGACAAATTCATCTCAGCATCAGCAGCTGCAGCCT	373
Qy	241	GAAGATTTCCTACTTACTTTGTCAACAGTCTGACAGTTGGCGATCAGCTTGGCCAA	300
Db	374	GAAGATTTCGCAACTTATTTGTCAACAGGTAAACAGTTCCCGATCAGCTTGGCCAA	433
Qy	301	GGGACAGCACTGGACATTCAA	321
Db	434	GGGACAGCACTGGAGATTAA	454

Search completed: September 11, 2005, 22:50:42
 Job time : 2584.67 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 19:40:23 ; Search time 98,7318 Seconds
(without alignments)
5319.914 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 gggctccagatgaccagcgc.....ggagacagctggacattcaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
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6: /cgn2_6/prodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.8	75.0	321	3	US-09-240-274-106
2	236.2	73.6	321	2	US-08-378-939-13
3	231.4	72.1	720	4	US-09-192-854-1
4	228.2	71.1	714	4	US-09-472-087-62
5	224	69.8	321	3	US-09-240-274-216
6	223.2	69.5	321	3	US-09-240-274-102
7	223.2	69.5	321	3	US-09-240-274-109
8	223.2	69.5	321	3	US-09-240-274-215
9	223.2	69.5	321	3	US-09-240-274-217
10	223.2	69.5	321	3	US-09-240-274-218
11	221.8	69.1	974	4	US-09-859-053-29
12	221.6	69.0	321	3	US-09-240-274-199
13	220.2	68.6	388	3	US-09-042-353-358
14	220.2	68.5	388	3	US-08-758-417A-206
15	220	68.5	321	3	US-09-240-274-107
16	218.4	68.0	321	3	US-09-240-274-211
17	218.4	68.0	321	3	US-09-240-274-221
18	218.4	68.0	321	3	US-09-240-274-222
19	217.8	67.9	451	4	US-09-472-087-50
20	217	67.6	439	3	US-09-042-353-360
21	216.8	67.5	439	3	US-08-758-417A-208
22	216.8	67.5	439	3	US-09-240-274-201
23	216.2	67.4	672	4	US-09-456-090A-47
24	216.2	67.4	672	4	US-09-453-234-47
25	216	67.3	321	3	US-09-240-274-205
26	215.4	67.1	324	2	US-08-378-939-31
27	215.4	67.1	324	2	US-08-378-939-33

28	215.4	67.1	387	3	US-08-803-085-3	Sequence 3, Appl
29	215.4	67.1	19040	3	US-09-343-485A-3	Sequence 3, Appl
30	215.2	67.0	321	3	US-09-240-274-105	Sequence 105, Appl
31	215.2	67.0	321	3	US-09-240-274-113	Sequence 113, Appl
32	215.2	67.0	327	4	US-09-627-896B-25	Sequence 25, Appl
33	213.8	66.6	324	2	US-08-378-939-17	Sequence 17, Appl
34	213.8	66.6	420	3	US-09-042-353-420	Sequence 420, App
35	213.8	66.6	420	3	US-08-758-417A-220	Sequence 420, App
36	213.8	66.6	3819	3	US-09-042-353-393	Sequence 393, App
37	213.8	66.6	3819	3	US-08-758-417A-243	Sequence 243, App
38	213.6	66.5	321	3	US-09-240-274-108	Sequence 108, App
39	213.6	66.5	321	3	US-09-240-274-203	Sequence 203, Appl
40	213.6	66.5	402	4	US-09-472-087-49	Sequence 49, Appl
41	213.2	66.4	390	2	US-08-646-367-2	Sequence 2, Appl
42	212.2	66.1	321	1	US-08-488-376-12	Sequence 12, Appl
43	212.2	66.1	321	2	US-08-634-223-12	Sequence 12, Appl
44	212.2	66.1	321	2	US-08-634-224-12	Sequence 12, Appl
45	212.2	66.1	321	2	US-08-634-400-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-240-274-106
; Sequence 106, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 106
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 106
US-09-240-274-106
Query Match          75.0%; Score 240.8; DB 3; Length 321;
Best Local Similarity 85.1%; Pred No. 98-75; Mismatches 47; Indels 0; Gaps 0;
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 6 CAGATGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAATCAG 65
DB 3 CAGGTGACCCAGTCTCCATCTCCCTGTCGATCTGTAGAGACAGAGTCAATCAG 62
QY 66 TTGCGGGGAGATCAGAGATTAAGATTAATGTATCAGCAGAAACAGAGACA 125
DB 63 TTGCGGGGAGATCAGAGATTAAGATTAATGTATCAGCAGAAACAGAGACA 122
QY 126 GCCTCTAAGCTGATCTTATTAATGAGGAGATCCGAGGAGATCCCTGACGATT 185
DB 123 AGCCCTAAGCTGATCTTATTAATGAGGAGATCCGAGGAGATCCCTGACGATT 182
QY 186 CAGCGGAGATGATCTGGAGCAATTAATCACTCCATCAGATCAGACCTGACGAGA 245
DB 183 CAGTGGAGATGATCTGGAGCAATTAATCACTCCATCAGATCAGACCTGACGAGA 242
QY 246 TTTCGCTACTTACTTTTGCAACAGTTCGACAGTTTGGCCAGTCTGGCAGAGAC 305
DB 243 TTTCGCTACTTACTTTTGCAACAGTTCGACAGTTTGGCCAGTCTGGCAGAGAC 302
QY 306 ACGACTGACATTTCAA 321
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Db 303 ACGACTGGAGATTAAA 318

RESULT 2

US-08-378-939-13
Sequence 13, Application US/08378939

Patent No. 5876961

GENERAL INFORMATION:

APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

STREET: 555 THIRTEENTH ST. N.W.

CITY: WASHINGTON

STATE: D. C.

COUNTRY: U. S.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,939

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..321

US-08-378-939-13

Query Match 73.6%; Score 236.2; DB 2; Length 321;

Best Local Similarity 83.5%; Pred. No. 3.8e-73;

Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Db 1 GAGCTCCAGATGACCCAGTCTCATCTCCCTGTCTGATCTGTAGAGACAGAGTCAAC 60

Db 1 GACATTCAGATGACCCAGTCTCATCTCCCTGTCTGATCTGTAGAGACAGAGTCAAC 60

Qy 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGACAGCTATTAAATTTGGTATCAGAGAAACA 120

Db 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGACAGCTATTAAATTTGGTATCAGAGAAACA 120

Qy 121 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Db 121 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Qy 121 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Db 121 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Qy 181 CGATTGAGGGGCAAGTAACTGGGCAAAATTACACTCTACATCGACGACGCGTCAACCT 240

Db 181 CGATTGAGGGGCAAGTAACTGGGCAAAATTACACTCTACATCGACGACGCGTCAACCT 240

Qy 181 AGGTTCAAGTGGCAAGTGAATCTGGGACAGACTTCACTCAACATCGACGAGTCTGCAACT 240

Db 181 AGGTTCAAGTGGCAAGTGAATCTGGGACAGACTTCACTCAACATCGACGAGTCTGCAACT 240

Qy 241 GAAGATTTTGCTACTTACTTTTGTCAAGCTCTGACAGATTGCCGATCACTTCGGCCAA 300

Db 241 GAAGATTTTGCTACTTACTTACTTTTGTCAAGCTCTGACAGATTGCCGATCACTTCGGCCAA 300

Qy 301 GGGACACGACTGGACATTCAA 321

Db 301 GGGACACGACTGGAGATTAAA 321

RESULT 3

US-09-192-854-1

Sequence 1, Application US/09192854

Patent No. 6696245

GENERAL INFORMATION:

APPLICANT: Winter, Greg

APPLICANT: Tomlinson, Ian

TITLE OF INVENTION: Methods for Selecting Functional Peptides

FILE REFERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

CURRENT FILING DATE: 1998-11-17

EARLIER APPLICATION NUMBER: 60/066,729

EARLIER FILING DATE: 1997-11-21

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 720

TYPE: DNA

ORGANISM: Homo sapiens

US-09-192-854-1

Query Match 72.1%; Score 231.4; DB 4; Length 720;

Best Local Similarity 82.6%; Pred. No. 2.9e-71;

Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1 GAGCTCCAGATGACCCAGTCTTCATCTCCCTGTCTGATCTGTAGAGACAGAGTCAAC 60

Db 397 GACATTCAGATGACCCAGTCTTCATCTCCCTGTCTGATCTGTAGAGAGAGAGTCAAC 456

Qy 61 ATCACTTGGCCGGGCAAGTCAAGACATTAGACAGCTATTAAATTTGGTATCAGAGAAACA 120

Db 457 ATCACTTGGCCGGGCAAGTCAAGACATTAGACAGCTATTAAATTTGGTATCAGAGAAACA 120

Qy 121 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Db 517 GGAAGAGCTCTTAAGTCTCTATTACTGGGCACTTCAACCCGGGAATCCGGGGTCCCTGAC 180

Qy 181 CGATTGAGGGGCAAGTAACTGGGCAAAATTACACTCTACATCGACGACGCTGACGCT 240

Db 577 AGGTTCAAGTGGCAAGTGAATCTGGGACAGATTGACCTCAACATCGACGAGTCTGCAACT 636

Qy 241 GAAGATTTTGCTACTTACTTTTGTCAAGCTCTGACAGATTGCCGATCACTTCGGCCAA 300

Db 637 GAAGATTTTGCTACTTACTTACTTTTGTCAAGCTCTGACAGATTGCCGATCACTTCGGCCAA 300

Qy 301 GGGACACGACTGGACATTCAA 321

Db 697 GGGACACGACTGGAAATCAA 717

Qy 301 GGGACACGACTGGACATTCAA 321

Db 697 GGGACACGACTGGAAATCAA 717

Qy 301 GGGACACGACTGGACATTCAA 321

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Db 697 GGGACACGACTGGAAATCAA 717

Qy 301 GGGACACGACTGGACATTCAA 321

Db 697 GGGACACGACTGGAAATCAA 717

CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 714
TYPE: DNA
ORGANISM: Homo sapiens
US-09-472-087-62

Query Match 71.1%; Score 228.2; DB 4; Length 714;
Best Local Similarity 81.9%; Pred. No. 3,9e-70;
Matches 253; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGCACTCTGTAGAGACAGAGTACC 60
DB 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTGCACTCTGTAGAGACAGAGTACC 126
QY 61 ATCACTTCCGGGAGAGTACAGACATTAGACAGTATTAAATTGTATCAGCAAGAACCA 120
DB 127 ATCACTTCCGGGAGAGTACAGACATTAGACAGTATTAAATTGTATCAGCAAGAACCA 186
QY 121 GGACAGCTCTCTAGCTGCTATTATCTGGGCACTACCCGGGAATCCGGGATCCCTGAC 180
DB 187 GGGAAAGCCCTTAATCTCTGATCTATGCTGCACTTCCAGTTGCAAGTGGGTCCTATCA 246
QY 181 CGATTGAGGGGAGTGAATCTGGGACAAATTACACTTCCATCCATCAGACGCTGACGCT 240
DB 247 AGGTTGAGTGGCAGTGGATCTGGGACAGATTTCACCTCAGCAGCTGCAACCT 306
QY 241 GAAGATTTGCTACTTCTTTGTCAACAGTCTGAGAGTTGGCCATCCTTGGGCCAA 300
DB 307 GAAGATTTGCACTTACTACTGCTCAACAGTATTACAGTACTTCACTTTCGGCCCT 366
QY 301 GGGACAGACTGGACATTCA 321
DB 367 GGGACCAAGTGAATCAAA 387

RESULT 5
US-09-240-274-216
Sequence 216, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 216
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-240-274-216

Query Match 69.8%; Score 224; DB 3; Length 321;
Best Local Similarity 82.4%; Pred. No. 7,7e-69;
Matches 257; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 6 CGAGATGACCCAGTCT 65
DB 3 CGAGTCAACCCAGTCT 62

QY 66 TTGCGGGGCAAGTCAAGATTTAGAGCTATTAAATTGTTATCAGCAAGAACAGAGCA 125
DB 63 TTGCGGGGCAAGTCAAGATTTAGAGCTATTAAATTGTTATCAGCAAGAACAGAGCA 122
QY 126 GCTCTTAAGTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGATCCCTGACGATT 185
DB 123 AGCCCTTAACCTCTGATCTATGCTGCACTTCCAGTTGCAAGTGGGGTCCCATCAAGTT 182
QY 186 CAGCGGCAAGTGAATCTGGGACAAATTACACTCTCAGCATCAGACCTGCAAGCTGAAGA 245
DB 183 CAGTGGCAGTGAATCTGGGACAGATTTCACCTCAGCATCAGACCTGCAAGCTGAAGA 242
QY 246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTGGCGAATCAGCTTCGGCAAGGAC 305
DB 243 TTTTGCACTTACTTCTGTCAACAGATTACAGTTATCTCGCAGCTTCGGCAAGGAC 302
QY 306 ACGACTGACAT 317
DB 303 CAGGTTGAGAT 314

RESULT 6
US-09-240-274-102
Sequence 102, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 102
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-102

Query Match 69.5%; Score 223.2; DB 3; Length 321;
Best Local Similarity 81.6%; Pred. No. 1,5e-68;
Matches 258; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 6 CGAGATGACCCAGTCT 65
DB 3 CGAGTCAACCCAGTCT 62
QY 66 TTGCGGGGCAAGTCAAGATTTAGAGCTATTAAATTGTTATCAGCAAGAACAGAGCA 125
DB 63 TTGCGGGGCAAGTCAAGATTTAGAGCTATTAAATTGTTATCAGCAAGAACAGAGCA 122
QY 126 GCTCTTAAGTGTCTATTACTGTGGCATCTACCCGGGAATCCGGGATCCCTGACGATT 185
DB 123 AGCCCTTAACCTCTGATCTATGCTGCACTTCCAGTTGCAAGTGGGGTCCCATCAAGTT 182
QY 186 CAGCGGCAAGTGAATCTGGGACAAATTACACTCTCAGCATCAGACCTGCAAGCTGAAGA 245
DB 183 CAGTGGCAGTGAATCTGGGACAGATTTCACCTCAGCATCAGACCTGCAAGCTGAAGA 242
QY 246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTGGCGAATCAGCTTCGGCAAGGAC 305
DB 243 TTTTGCACTTACTTCTGTCAACAGATTACAGTTATCTCGCAGCTTCGGCAAGGAC 302
QY 306 ACGACTGACATTCA 321

Db 63 TTGCGGGGCAAGTCAGTACATAGCAGTATTAATGGTATCAGAGAAACAGGAA 122
126 GCCTCTAAGCTGCTCATTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACCGATT 185
Db 123 AGCCCTTAATCTCTATCTATCTGCTCATCCAGTTTGGCAAGTGGGTCCTCATCAAGGTT 182
Qy 186 CAGCGGCAAGTATCTGGGCAAAATTAACCTCACCATCAGAGGCTGACGCTGAAGA 245
Db 183 CAGTGGCAGTATCTGGGCAAGATTTCACTCACCATCAGAGTCTGCAACCTGAAGA 242
Qy 246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACCTTGGCCCAAGGAC 305
Db 243 TTTTGCAACTTACTACTGTCAACAGATTACAGTTCCCTGACACTTTGGCCCTGGAC 302
Qy 306 ACGACTGACATTCAA 321
Db 303 CAAGTGAGATATCAAA 318

RESULT 10

US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

Query Match 69.5%; Score 223.2; DB 3; Length 321;
Best Local Similarity 81.6%; Pred. No. 1.5e-68;
Matches 258; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 6 CCAGATGACCCAGTCTCCATCTCCCTGCTGATGCTAGAGACAGATCACCATCAC 65
Db 3 CAGAGTCAACCCAGTCTCCATCTCCCTGCTGATGCTAGAGACAGATCACCATCAC 62
Qy 66 TTGCGGGGCAAGTCAGAGATTAAGCAGCTAATTAATGGTATCAGAGAAACAGAGACA 125
Db 63 TTGCGGGGCAAGTCAGAGATTAAGCAGCTAATTAATGGTATCAGAGAAACAGAGACA 122
Qy 126 GCCTCTAAGCTGCTCATTTACTGGGATCTACCCGGGATCCGGGGTCCCTGACCGATT 185
Db 123 AGCCCTTAATCTCTATCTATCTGCTCATCCAGTTTGGCAAGTGGGTCCTCATCAAGGTT 182
Qy 186 CAGCGGCAAGTATCTGGGCAAAATTAACCTCACCATCAGAGGCTGACGCTGAAGA 245
Db 183 CAGTGGCAGTATCTGGGCAAGATTTCACTCACCATCAGAGTCTGCAACCTGAAGA 242
Qy 246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACCTTGGCCCAAGGAC 305
Db 243 TTTTGCAACTTACTACTGTCAACAGATTACAGTTCCCTGACACTTTGGCCCTGGAC 302
Qy 306 ACGACTGACATTCAA 321
Db 303 CAAGTGAGATATCAAA 318

RESULT 11

US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match 69.1%; Score 221.8; DB 4; Length 974;
Best Local Similarity 80.7%; Pred. No. 8.3e-68;
Matches 259; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1 GAGCTTCAGATGATACCCAGTCTCCATCTCCCTGCTGATGCTAGAGACAGATCACC 60
Db 105 GACATTCAGATGATACCCAGTCTCCATCTCCCTGCTGATGCTAGAGACAGATCACC 164
Qy 61 ATCAGTTCGCGGGCAAGTCAGAGATTAAGCAGCTAATTAATGGTATCAGAGAAACA 120
Db 165 ATCAGTTCGCGGGCAAGTCAGAGATTAAGCAGCTAATTAATGGTATCAGAGAAACA 224
Qy 121 GAGAGCCTCTTAAGCTGCTCATTTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 180
Db 225 GGGAAAGCCCTTAAGCTGCTCATTTACTGGGATCTACCCGGGAAATCCGGGGTCCCTGAC 284
Qy 181 CGATTGAGCGGCAAGTATCTGGGCAAAATTAACCTCACCATCAGAGGCTGACGCT 240
Db 285 AGTTTCAGCGGCAAGTATCTGGGCAAAATTAACCTCACCATCAGAGGCTGACGCT 344
Qy 241 GAAAGTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACCTTGGCCCA 300
Db 345 GAAAGTTTGTACTTACTTTTGTCAACAGTCTGACAGTTGGCCGATCACCTTGGCCCA 404
Qy 301 GGGACAGAGTGGACATTCAA 321
Db 405 GGGACAGAGTGGAAATCAAA 425

RESULT 12

US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202

1 CURRENT APPLICATION NUMBER: US/09/240,274
2 CURRENT FILING DATE: 1999-01-29
3 EARLIER APPLICATION NUMBER: 60/081,380
4 EARLIER FILING DATE: 1998-04-10
5 EARLIER APPLICATION NUMBER: 60/028,550
6 EARLIER FILING DATE: 1996-10-11
7 NUMBER OF SEQ ID NOS: 224
8 SOFTWARE: Patent Ver. 2.0
9 SEQ ID NO 199
10 LENGTH: 321
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 OTHER INFORMATION: anti-Rh(D) antibody clone SH13
15 US-09-240-274-199

Query Match 69.0%; Score 221.6; DB 3; Length 321;
Best Local Similarity 81.3%; Pred. No. 5,4e-68;
Matches 257; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCCCTCCTGTCGATCTGTAGAGACAGAGTACCATCAG 65
DB 3 CAGAGTCACCCAGTCTCCATCCCTCCTGTCGATCTGTAGAGACAGAGTACCATCAG 62
QY 66 TTGCGCGGAGAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGACAGAAACAGACA 125
DB 63 TTGCGCGGAGAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGACAGAAACAGACA 122
QY 126 GCCTCTTAAAGTCTCTATTACTGGGCACTTACCCGGGAATCCGGGGTCCCTGACCGATT 185
DB 123 AGCCCTTAAGCTCTTATCTATCTAGCTGCACTCCAGTTTGGCAAGGGGTCCCATCAAGGTT 182
QY 186 CAGCGGAGTGAATCTGGGACAAATTACACTCTCACCATCAGAGCGCTCAGCTGAGA 245
DB 183 CAGTGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGAGCGCTCAGCTGAGA 242
QY 246 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCCTGCGCCAAAGGAC 305
DB 243 TTTTGTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCCCTGCGCCAAAGGAC 302
QY 306 ACGACTGACATTCAA 321
DB 303 CAGCTGGAGATCAAA 318

RESULT 13
US-09-042-353-358
Sequence 358, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279

1 FILING DATE: 17-DEC-1991
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 07/853,408
4 FILING DATE: 18-MAR-1992
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 07/904,068
7 FILING DATE: 23-JUN-1992
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 07/990,860
10 FILING DATE: 16-DEC-1992
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/053,131
13 FILING DATE: 26-APR-1993
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/096,762
16 FILING DATE: 22-JUL-1993
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/155,301
19 FILING DATE: 18-NOV-1993
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/161,739
22 FILING DATE: 03-DEC-1993
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/165,699
25 FILING DATE: 10-DEC-1993
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/209,741
28 FILING DATE: 09-MAR-1994
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/352,322
31 FILING DATE: 07-DEC-1994
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 08/544,404
34 FILING DATE: 10-OCT-1995
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 08/728,463
37 FILING DATE: 10-OCT-1996
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: WO PCT/US96/16433
40 FILING DATE: 10-OCT-1996
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: US 08/758,417
43 FILING DATE: 02-DEC-1996
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: WO PCT/US97/21803
46 FILING DATE: 01-DEC-1997
47 ATTORNEY/AGENT INFORMATION:
48 NAME: Apple, Randolph T.
49 REGISTRATION NUMBER: 36,429
50 REFERENCE/DOCKET NUMBER: 014643-009040US
51 TELEPHONE: (415) 576-0200
52 TELEFAX: (415) 576-0300
53 INFORMATION FOR SEQ ID NO: 358:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 388 base pairs
56 TYPE: nucleic acid
57 STRANDEDNESS: single
58 TOPOLOGY: linear
59 MOLECULE TYPE: DNA
60 US-09-042-353-358

Query Match 68.6%; Score 220.2; DB 3; Length 388;
Best Local Similarity 80.4%; Pred. No. 1.9e-67;
Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 GAGCTCGAGTACCCAGTCTTCATCTCCCTGTCGATCTGTAGAGACAGAGTACCC 60
DB 67 GAGATTCAGATGACCCAGTCTTCATCTCCCTGTCGATCTGTAGAGACAGAGTACCC 126
QY 61 ATCACTTCCCGGAGAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGACAGAAACCA 120
DB 127 ATCACTTCCCGGAGAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGACAGAAACCA 186

QY 121 GGACAGCTCTAGCTGCTCATTTTCTGGGCATCTACCCGGGAATCCGGGTCCTGCAC 180
DB 187 GGGAAAGCCCCCTAGCTCCGATCTGATCTGCTGATCCGATTGGAAGTGGGTCCTCATCA 246
QY 181 CGATTGAGCGGAGTGAATCTGGGACAAATTACACTCTCCACATCAGCAGCTGCAGCCT 240
DB 247 AGCTTCAGCGGAGTGAATCTGGGACAGATTTCACCTCTCCATCAGCAGCTGCAGCCT 306
QY 241 GAAGATTTTGTCTACTTCTTTTGTCAACAGCTGACAGTTTGGCCGATCAGCTTGGCCAA 300
DB 307 GAAGATTTTGTCACTTACTTGTCAACAGGCTAATAGTTCCCGTACACTTTTGGCCAG 366
QY 301 GGGACAGACTGACATTCAA 321
DB 367 GGGACCAAGCTGGAGATCAAA 387

RESULT 14
US-08-758-417A-206
Sequence 206, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomberg, Nile
KAY, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antidodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

Query Match 68.6%; Score 220.2; DB 3; Length 388;
Best Local Similarity 80.4%; Pred. No. 1.9e-67;
Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 GAGCTCCAGATGATACCCAGTCTTCCATCTCCCTGCTGCACTCTGTAGAGAGAGAGTCCAC 60
DB 67 GACATTCAGATGATACCCAGTCTTCCATCTCTCCCTGCTGCACTCTGTAGAGAGAGAGTCCAC 126
QY 61 ATCACTTGGCGGGCAAGTGAAGAGATTAAGAGATTAATTTGATGAGAGAGAGAGAGAGAG 120
DB 127 ATCACTTGGCGGGCAAGTGAAGAGATTAAGAGATTAATTTGATGAGAGAGAGAGAGAGAG 186
QY 121 GGAAGCTCTCTAGCTGCTCATTTTCTGGGCAATCCCGGAATCCGGGTCCTGCAC 180
DB 187 GGGAAAGCCCCCTAAGCTCTGATCTATGCTGATCCAGTTCAGAAAGTGGGTCCTCATCA 246
QY 181 CGATTGAGCGGAGTGAATCTGGGACAAATTACACTCTCCACATCAGCAGCTGCAGCCT 240
DB 247 AGCTTCAGCGGAGTGAATCTGGGACAGATTTCACCTCTCCATCAGCAGCTGCAGCCT 306
QY 241 GAAGATTTTGTCTACTTCTTTTGTCAACAGCTGACAGTTTGGCCGATCAGCTTGGCCAA 300
DB 307 GAAGATTTTGTCACTTACTTGTCAACAGGCTAATAGTTCCCGTACACTTTTGGCCAG 366
QY 301 GGGACAGACTGACATTCAA 321
DB 367 GGGACCAAGCTGGAGATCAAA 387

RESULT 15
US-09-240-274-107
Sequence 107, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 107
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 107
US-09-240-274-107

Query Match 68.5%; Score 220; DB 3; Length 321;
Best Local Similarity 81.0%; Pred. No. 2e-67;
Matches 256; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 6 CGAGATGACCGAGTCTTCCATCTCTCTGCTGCACTCTGTAGAGAGAGAGATCAATCCAC 65
DB 3 CGAGCTCACCCAGTCTTCCATCTCTCTGCTGCACTCTGTAGAGAGAGAGATCAATCCAC 62
QY 66 TTGCGGGCAAGTCAAGATGAGAGATTAATTTGATGAGAGAGAGAGAGAGAGAGAGAGAG 125

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Db      63 TTGCGGGCAAGTCAGAGCATTAGCAGTATTTAATTGATACAGAGAAACAGGGAA 122
Qy      126 GCCTCCTTAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGCTCCTGACCGATT 185
Db      123 AGCCCTTAGCTCCTGATCTATGCTGCAATCCAGTTTGCAAGTGGGTCCTCATCAAGGTT 182
Qy      186 CAGCGGCACTGAATCTGGGACAATTTACACTCTCACCATCAGCAGCCTGCAGCTGAAGA 245
Db      183 CAGTGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGTCTGCAACTGAAGA 242
Qy      246 TTTTGCTACTTACTTTTGCAACAGTCTGACAGTTTGCCGATCACCCTTGCGGCCAAGGGAC 305
Db      243 TTTTGCACTTACTACTGTCAACAGATTACAGTACCCTCGAATTTCGGCGAGGGGAC 302
Qy      306 ACGACTGGACATTCAA 321
Db      303 CAAGGTGGAGATCAAA 318

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 11, 2005, 21:22:08 / Search time 508.25 Seconds
(without alignments)
4147.731 Million cell updates/sec

Title: US-09-403-107-147

Perfect score: 321

Sequence: 1 gagctccagatgaccagctc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

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Maximum DB seq length: 200000000

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Maximum Match 100%

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Database: Published Applications NA.*

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22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	15	US-10-325-694-147
2	255.4	79.6	321	15	US-10-325-694-141
3	245.8	76.6	324	19	US-10-344-514-7
4	245.8	76.6	324	19	US-10-344-514-8
5	240.8	75.0	321	10	US-09-848-798-106
6	240.2	74.8	321	19	US-10-703-714-11
7	240.2	74.8	321	19	US-10-703-714-19

8	239.4	74.6	322	17	US-10-309-762-215	Sequence 215, App
9	239.4	74.6	322	17	US-10-309-762-228	Sequence 228, App
10	237.8	74.1	321	21	US-10-727-155-155	Sequence 155, App
11	236.2	73.6	321	21	US-10-727-155-141	Sequence 141, App
12	236.2	73.6	321	21	US-10-727-155-159	Sequence 159, App
13	236.2	73.6	322	17	US-10-309-762-213	Sequence 213, App
14	236.2	73.6	322	17	US-10-309-762-238	Sequence 238, App
15	236.2	73.6	458	21	US-10-644-277-55	Sequence 55, App
16	235	73.2	1106	17	US-10-264-049-121	Sequence 121, App
17	233	72.6	321	21	US-10-727-155-149	Sequence 149, App
18	233	72.6	321	21	US-10-949-135-25	Sequence 25, App
19	231.4	72.1	333	16	US-10-203-754A-60	Sequence 60, App
20	231.4	72.1	720	9	US-09-192-854-1	Sequence 1, Appl
21	231.4	72.1	720	9	US-09-968-561A-1	Sequence 1, Appl
22	231.4	72.1	720	10	US-09-968-561A-1	Sequence 1, Appl
23	231.4	72.1	720	11	US-09-968-561A-1	Sequence 1, Appl
24	231.4	72.1	720	20	US-10-744-774-2	Sequence 2, Appl
25	231.4	72.1	900	16	US-10-203-754A-64	Sequence 64, Appl
26	230.4	71.8	321	21	US-10-949-135-9	Sequence 9, Appl
27	229.8	71.6	321	17	US-10-338-366-11	Sequence 11, Appl
28	229.8	71.6	322	22	US-10-916-840-115	Sequence 115, App
29	229.8	71.6	324	19	US-10-344-514-3	Sequence 3, Appl
30	229.8	71.6	324	19	US-10-344-514-4	Sequence 4, Appl
31	229.8	71.6	729	15	US-10-216-484-125	Sequence 125, App
32	229.8	71.6	729	16	US-10-384-933-125	Sequence 125, App
33	229.6	71.5	348	22	US-10-916-758-40	Sequence 40, Appl
34	228.2	71.1	322	17	US-10-309-762-226	Sequence 226, App
35	228.2	71.1	322	17	US-10-309-762-227	Sequence 227, App
36	228.2	71.1	324	20	US-10-409-814A-3	Sequence 3, Appl
37	228.2	71.1	405	21	US-10-783-311-15	Sequence 15, Appl
38	228.2	71.1	405	21	US-10-783-311-16	Sequence 16, Appl
39	228.2	71.1	702	21	US-10-938-353-3	Sequence 3, Appl
40	228.2	71.1	714	14	US-10-153-382-18	Sequence 18, Appl
41	228.2	71.1	714	20	US-10-612-497-62	Sequence 62, Appl
42	228.2	71.1	714	20	US-10-776-649-62	Sequence 62, Appl
43	228.2	71.1	819	14	US-10-158-646-55	Sequence 65, Appl
44	226.6	70.6	322	16	US-10-041-860-74	Sequence 74, Appl
45	226.6	70.6	322	17	US-10-309-762-221	Sequence 221, App

ALIGNMENTS

RESULT 1
US-10-325-694-147
; Sequence 147, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-147

Query Match 100.0%; Score 321; DB 15; Length 321;
Best Local Similarity 100.0%; Pred. No. 3,38-101; Indels 0; Gaps 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTTCATCTCCCTGTGCAATCTGTAAGAGACAGACTCAC 60
DB 1 GAGCTCCAGATGACCCAGTCTTCATCTCCCTGTGCAATCTGTAAGAGAGACAGACTCAC 60

QY	61	ATCATTTGGCCGGGCAAGTCAGAGCAATTACAGCTATTTAAATTGGATATCAGCAGAAACCA	120
Db	61	ATCATTTGGCCGGGCAAGTCAGAGCAATTACAGCTATTTAAATTGGATATCAGCAGAAACCA	120
QY	121	GGACAGCCTCTTAAGCTGTCTATTAACTGGGGAATCTAACCCGGGGAATCCGGGGTCCCTGAC	180
Db	121	GGACAGCCTCTTAAGCTGTCTATTAACTGGGGAATCTAACCCGGGGAATCCGGGGTCCCTGAC	180
QY	181	CGATTACAGCGGAGTGAATCTGGGCAAAATTTCACCTCAGCATACAGAGCCTGAGAGCCT	240
Db	181	CGATTACAGCGGAGTGAATCTGGGCAAAATTTCACCTCAGCATACAGAGCCTGAGAGCCT	240
QY	241	GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCGATCACTTTGGCCCAA	300
Db	241	GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCGATCACTTTGGCCCAA	300
QY	301	GGGACACAGCTGGACATTTCAA	321
Db	301	GGGACACAGCTGGACATTTCAA	321

```

RESULT 2
US-10-325-694-141
; Sequence 141, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUW, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-141

```

Query Match	79.6%;	Score 255.4;	DB 15;	Length 321;
Best Local Similarity	87.2%;	Pred. No. 2.5e-78;		
Matches 280;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;

OY	1	TAGCTTCACAATATACCCAGATCTCCATCTCCGCTGTGACATCTGTAGAGACAAGTACCC	60
Db	1	GAGCTTCAGATATACCCAGATCTCCATCTCCGCTGTGACATCTGTGAGAGACAAGTACCC	60
OY	61	ATCATCTTGCCTGGGCAAGTCAGAGCATTTAGCAGTAAATTTGATATGCAAGAAACCA	120
Db	61	ATCATCTTGTTCGACCAAGTCAGAGCATTTAGCAGTAAATTTGATATGCAAGAAACCA	120
OY	121	GGACAGCCCTCCTTAGCTGCTCAATTTTACTGGGCACTTACCCGGGAATCCGGGGATCCCTGAC	180
Db	121	GGACAGCCCTCCTTAGCTGCTCAATTTTACTGGGCACTTACCCGGGAATCCGGGGATCCCTGAC	180
OY	181	CGATTTCAGCGGCAAGTGAATCTGGGACAAATTTACCTCTCCATCAGACAGCCTTGACGCTT	240
Db	181	CGATTTCAGTGGGACGCGGCTCTGGGACAGATTTACTCTCACTCAGCAGTCTTACAACTT	240
OY	241	GAAGATTTTGGTACTACTTTTGTCAACAGTCTGACAGATTTTGGCGATCACTTCGGGCAA	300
Db	241	GAGATTTCTGCAACTTACTACTGTACGACAGATTAGCAATCCCCGTACACTTTTGGGCAAG	300
OY	301	GGGACACGACTGGACATTTCAA	321
Db	301	GGGACCAAGCTGGAGATCAA	321

```

US-10-344-514-7
; Sequence 7, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
; APPLICANT: NAKASHIMA, Toshihiro et al.
; TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
; FILE REFERENCE: 0020-5111P
; CURRENT APPLICATION NUMBER: US/10/344,514
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP 2001-177640
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 7
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-514-7

Query Match          76.6%;   Score 245.8;   DB 19;   Length 324;
Best Local Similarity 85.4%;   Fred. No. 5.6e-75;
Matches 274;   Conservative 0;   Mismatches 47;   Indels 0;   Gaps 0

```

OY	1	GACCTCCAAATGACCCAGCTCCTCAATCCCTCGTGTGATCTGTAGGAGACAGATGACC	60
Db	1	GACATCCAGTTGACCCAGTCTCATCTCTCCCTGTGTATCTGTAGGAGACAGATGACC	60
OY	61	ATCACTTGGCCGGGACAGTCAGAGCATTTAGACATTTAAATTGTATTCAGCAAAACCA	120
Db	61	ATCACTTGGCCGGGCAAGTCAGAGCATTTAGACATTTAAATTGTATTCAGCAAAACCA	120
OY	121	GGACAGCCTCTTAAGTGTCTAATTATCTGGGATCTACCCGGGAATCCGGGGTCCCTGAC	180
Db	121	GGAAAGCCCCCTTAAGTCTCTGATCTAATGTGTGATCAAGATTTGCAAAGTGGGGTCCATCA	180
OY	181	CGATTCAGCGGAGTGAATCTGGGACAAATTACACTTCACCATCAGCAGCGCTCGACCT	240
Db	181	AGGTTCAAGTGGCAGGTGGAATCTGGGACAAATTTCACTTCAACATCAGGAAGTCTCAACT	240
OY	241	GAAGATTTTGTCTACTTACTTTGTCAACAGTCTGACAGTTTGGCGATCACCTTGGGCCAA	300
Db	241	GAAGATTTTGTCAACTTACTACTGTCAACAGATTTACAGTACCCGATCACCTTGGGCCAA	300

Oy 301 GGGACACGACTGGACATTCAA 321
|||
Db 301 GGGACACGACTGGAGATTAA 321

```

RESULT 4
US-10-344-514-8
; Sequence 8, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
; APPLICANT: NAKASHIMA, Toshihiro et al.
; TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
; FILE REFERENCE: 0020-511P
; CURRENT APPLICATION NUMBER: US/10/344, 514
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP 2001-177640
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 8
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (324)
US-10-344-514-8

```

Query Match	76.6%;	Score 245.8;	DB 19;	Length 324;
Best Local Similarity	85.4%;	Pred. No. 5.6e-75;		
Matches 274;	Conservative 0;	Mismatches 47;	Indels 0;	Gaps 0

PRIOR FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(321)
US-10-703-714-19

Query Match 74.8%; Score 240.2; DB 19; Length 321;
Best Local Similarity 84.9%; Pred. No. 5e-73;
Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 TTCAGATGACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCATCA 64
DB 5 TCCAGTTGACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCATCA 64
QY 65 CTTGCCGGGCAAGTCAGAGCATTTAGAGCATTTAAATTGTTATCGAGAAACCGAGAC 124
DB 65 CTTGCCGGGCAAGTCAGAGCATTTAGAGCATTTAGAGCATTTAAATTGTTATCGAGAAACCGAGAC 124
QY 125 AGCCTCTAAGCTGCTCATTTACTGGGCACTTACCCGGGATCCGGGTCCCTGACCGAT 184
DB 125 AGCCTCTAAGCTGCTCATTTACTGGGCACTTACCCGGGATCCGGGTCCCTGACCGAT 184
QY 185 TCAGCGGCGAGTGATCTGGGCAAAATTACACTTCAACATCAGACGCTTGACGCTGAAG 244
DB 185 TCAGCGGCGAGTGATCTGGGCAAAATTACACTTCAACATCAGACGCTTGACGCTGAAG 244
QY 245 ATTTGCTCTACTTCTTTGTCACACAGTCGAGCTTGGCGATCCGACCTCGGCAAGGGA 304
DB 245 ATTTGCTCTACTTCTTTGTCACACAGTCGAGCTTGGCGATCCGACCTCGGCAAGGGA 304
QY 305 CACGACTGGAGATTCAA 321
DB 305 CACGACTGGAGATTCAA 321

RESULT 8
US-10-309-762-215
Sequence 215, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 215
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-215

Query Match 74.6%; Score 239.4; DB 17; Length 322;
Best Local Similarity 84.1%; Pred. No. 9.5e-73;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GAGCTCCAGTACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCC 60
DB 1 GAGCTCCAGTACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCC 60

QY 61 ATCACTTCCGGGCAAGTCAGAGCATTTAGAGCATTTAAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTTCGGGCGAGTCAGAGTATTAGCATTTGGTTAACTGGTATCAGAGAAACCA 120
QY 121 GGACAGCCTCTTACGCTCTCATTTACTGGGATCTACCCGGGAATCCGGGATCCCTTAC 180
DB 121 GGGAAGCCCTTACGCTCTCATTTACTGGGATCTACCCGGGAATCCGGGATCCCTTAC 180
QY 181 CGATTACAGGGGAGAGTCTGGGCAAAATTACACTCCACATCAGAGGCTGAGGCT 240
DB 181 AGTTTCAGGGGAGAGTCTGGGCAAAATTACACTCCACATCAGAGGCTGAGGCT 240
QY 241 GAAAGATTTGCTACTTACTTTGTCACAGTCTGACAGATTTGCCGATCACCCTTGCCCAA 300
DB 241 GAAAGATTTGCAACTTACTTATTTGTCACAGGCTAACAGGCTTCCCTATCACCCTTGCCCAA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGAGATTAAA 321

RESULT 9
US-10-309-762-228
Sequence 228, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudae, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 228
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-228

Query Match 74.6%; Score 239.4; DB 17; Length 322;
Best Local Similarity 84.1%; Pred. No. 9.5e-73;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GAGCTCCAGTACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCC 60
DB 1 GAGCTCCAGTACCCAGTCTCCATCTCCCTGTGATCTGTAGAGACAGAGTCACCC 60
QY 61 ATCACTTCCGGGCAAGTCAGAGCATTTAGAGCATTTAAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTTCGGGCGAGTCAGAGTATTAGCATTTGGTTAACTGGTATCAGAGAAACCA 120
QY 121 GGACAGCCTCTTACGCTCTCATTTACTGGGATCTACCCGGGAATCCGGGATCCCTTAC 180
DB 121 GGGAAGCCCTTACGCTCTCATTTACTGGGATCTACCCGGGAATCCGGGATCCCTTAC 180
QY 181 CGATTACAGGGGAGAGTCTGGGCAAAATTACACTCCACATCAGAGGCTGAGGCT 240
DB 181 AGTTTCAGGGGAGAGTCTGGGCAAAATTACACTCCACATCAGAGGCTGAGGCT 240
QY 241 GAAAGATTTGCTACTTACTTTGTCACAGTCTGACAGATTTGCCGATCACCCTTGCCCAA 300
DB 241 GAAAGATTTGCAACTTACTTATTTGTCACAGGCTAACAGGCTTCCCTATCACCCTTGCCCAA 300
QY 301 GGGACACGACTGGACATTCAA 321
DB 301 GGGACACGACTGGAGATTAAA 321

```
RESULT 10
US-10-727-155-155
; Sequence 155, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
; APPLICANT: Raffaela Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-155-155

Query Match      74.1%; Score 237.8; DB 21; Length 321;
Best Local Similarity 83.8%; Pred. No. 3.4e-72;
Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY      1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGCACTGTGTAGAGACAGAGTCAAC 60
DB      1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTGTGCACTGTGTAGAGACAGAGTCAAC 60
QY      61 ATCACTTGGCCGGGAGTCAAGAGATTTAGAGCTATTAAATTGGTATCAGCAAAACA 120
DB      61 ATCACTTGGCCGGGAGTCAAGAGATTTAGAGCTATTAAATTGGTATCAGCAAAACA 120
QY      121 GGCAGAGCTCTTAAGCTGCTCACTTCTGGGCACTCAACCGGGAATCCGGGGTCCCTGAC 180
DB      121 GGGAAAGCCCCCTGAGGTCCTGATCTATGCTGCAATTCATTGCAAGTGGGGTCCCATCA 180
QY      181 CGATTGAGCGGAGTGAATCTGGGCAAAATTACACTCTGACATCAGACAGCTGACGCT 240
DB      181 AGGTTGAGTGGGAGTGAATCTGGGCAAAATTACACTCTGACATCAGACAGCTGACGCT 240
QY      241 GAAAGTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCCATCACTTTGGCCAA 300
DB      241 GAAAGTTTGTCAACTTACTACTGTCAACAGAGTTCCAGTACCTTACCTTGGCCAA 300
QY      301 GGGACACGACTGGACATTCAA 321
DB      301 GGGACACGACTGGAGATTAAA 321

RESULT 11
US-10-727-155-141
; Sequence 141, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
```

```
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
; APPLICANT: Raffaela Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-727-155-141

Query Match      73.6%; Score 236.2; DB 21; Length 321;
Best Local Similarity 83.5%; Pred. No. 1.2e-71;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY      1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGTGCACTGTGTAGAGACAGAGTCAAC 60
DB      1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTGTGCACTGTGTAGAGACAGAGTCAAC 60
QY      61 ATCACTTGGCCGGGAGTCAAGAGATTTAGAGCTATTAAATTGGTATCAGCAAAACA 120
DB      61 ATCACTTGGCCGGGAGTCAAGAGATTTAGAGCTATTAAATTGGTATCAGCAAAACA 120
QY      121 GGCAGAGCTCTTAAGCTGCTCACTTCTGGGCACTCAACCGGGAATCCGGGGTCCCTGAC 180
DB      121 GGGAAAGCCCCCTGAGGTCCTGATCTATGCTGCAATTCATTGCAAGTGGGGTCCCATCA 180
QY      181 CGATTGAGCGGAGTGAATCTGGGCAAAATTACACTCTGACATCAGACAGCTGACGCT 240
DB      181 AGGTTGAGTGGGAGTGAATCTGGGCAAAATTACACTCTGACATCAGACAGCTGACGCT 240
QY      241 GAAAGTTTGTCTACTTCTTTGTCAACAGTCTGACAGTTTGGCCATCACTTTGGCCAA 300
DB      241 GAAAGTTTGTCAACTTACTACTGTCAACAGAGTTCCAGTACCTTACCTTGGCCAA 300
QY      301 GGGACACGACTGGACATTCAA 321
DB      301 GGGACACGACTGGAGATTAAA 321

RESULT 12
US-10-727-155-159
; Sequence 159, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
```

```
/ APPLICANT: Raffaeella Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Gioiuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ TITLE OF INVENTION: FACTOR AND USES THEREOF
/ FILE REFERENCE: ABGENIX.073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/430729
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 159
/ LENGTH: 321
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-727-155-159
```

```
Query Match
Best Local Similarity 73.6%; Score 236.2; DB 21; Length 321;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
DB 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
QY 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
QY 121 GGACAGCTCTTAAGTGTCTATTTACTGTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGCCCTCGAATCTCGATCTATGCGCATTTAAATTTGGAAGTGGGGTCCCATCA 180
QY 181 CGATTAGCGGGCAGTGAATCTGGGCAAAATTACACTTCAACATCGACGCTCGACGCT 240
DB 181 AGGATCAGGGCGAGTGTGATCTGGGCAAGTTTCACTCTCAACATCGACGCTCGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGATTTGGCGATCCCTCGGCCAA 300
DB 241 GAAGATTTTGTCAACTTACTTCTTCAACAGATTTGCAAGATTTCCAGTACCTTCCGCGCA 300
QY 301 GGGACACGACTGGACATTTCA 321
DB 301 GGGACACGACTGGAGATTAA 321
```

```
RESULT 13
US-10-309-762-213
/ Sequence 213, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
/ APPLICANT: Guada, Jean
/ APPLICANT: Foltz, Jean
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
/ FILE REFERENCE: ABGENIX.027A
/ CURRENT APPLICATION NUMBER: US/10/309,762
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 60/337275
/ PRIOR FILING DATE: 2001-12-03
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 213
/ LENGTH: 322
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-309-762-213
```

```
Query Match
Best Local Similarity 73.6%; Score 236.2; DB 17; Length 322;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
DB 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
QY 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
QY 121 GGACAGCTCTTAAGTGTCTATTTACTGTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGCCCTCGAATCTCGATCTATGCGCATTTTGAAGTGGGGTCCCATCA 180
QY 181 CGATTAGCGGGCAGTGAATCTGGGCAAAATTACACTTCAACATCGACGCTCGACGCT 240
DB 181 AGGATCAGGGCGAGTGTGATCTGGGCAAGTTTCACTCTCAACATCGACGCTCGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGATTTGGCGATCACCCTTGGCCAA 300
DB 241 GAAGATTTTGTCAACTTACTTCTTCAACAGATTTGCAAGATTTCCAGTACCTTCCGCGCA 300
QY 301 GGGACACGACTGGACATTTCA 321
DB 301 GGGACACGACTGGAGATTAA 321
```

```
RESULT 14
US-10-309-762-238
/ Sequence 238, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
/ APPLICANT: Guada, Jean
/ APPLICANT: Foltz, Jean
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
/ FILE REFERENCE: ABGENIX.027A
/ CURRENT APPLICATION NUMBER: US/10/309,762
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 60/337275
/ PRIOR FILING DATE: 2001-12-03
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 238
/ LENGTH: 322
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-309-762-238
```

```
Query Match
Best Local Similarity 73.6%; Score 236.2; DB 17; Length 322;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
```

```
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
DB 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTGTAGAGACAGAGTCACC 60
QY 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
DB 61 ATCACTTGGCCGGGCAAGTCAAGCATTTAGAGCATTAATTGGTATCAGAGAAACCA 120
QY 121 GGACAGCTCTTAAGTGTCTATTTACTGTGGGCACTTACCCGGGAATCCGGGGTCCCTGAC 180
DB 121 GGGAAGCCCTCGAATCTCGATCTATGCGCATTTTGAAGTGGGGTCCCATCA 180
QY 181 CGATTAGCGGGCAGTGAATCTGGGCAAAATTACACTTCAACATCGACGCTCGACGCT 240
DB 181 AGGATCAGGGCGAGTGTGATCTGGGCAAGTTTCACTCTCAACATCGACGCTCGACGCT 240
QY 241 GAAGATTTTGTCTACTTCTTTGTCAACAGTCTGACAGATTTGGCGATCACCCTTGGCCAA 300
DB 241 GAAGATTTTGTCAACTTACTTCTTCAACAGATTTGCAAGATTTCCAGTACCTTCCGCGCA 300
```

Db 241 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAACAGTTTCCTATACCTTGGGCCAA 3000

Qy 301 GGGACACGACTGACATTTCAA 321
|||||
301 GGGACACGACTGGAGATTAAA 321

Db

RESULT 15

```

US-10-644-277-55
: Sequence 55. Application US/106644277
: Publication No. US20050058639A1
: GENERAL INFORMATION:
: APPLICANT: Gudus, Jean M.
: APPLICANT: Haak-Frendescho, Mary
: APPLICANT: Poord, Orlit
: APPLICANT: Liang, Meina L.
: APPLICANT: Ahluwalia, Kiran
: APPLICANT: Bhakta, Sunil
: TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
: TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
: FILE REFERENCE: ABGEIX. 091A
: CURRENT APPLICATION NUMBER: US/10/644,277
: CURRENT FILING DATE: 2003-08-19
: PRIOR APPLICATION NUMBER: 60/404,802
: PRIOR FILING DATE: 2002-08-19
: NUMBER OF SEQ ID NOS: 149
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 55
: LENGTH: 458
: TYPE: DNA
: ORGANISM: Homosapien
: US-10-644-277-55

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Query Match	73.6%	Score 236.2;	DB 21;	Length 458;
Best Local Similarity	83.5%	Pred. No. 1.4e-71;		
Matches 268; Conservative	0;	Mismatches 53;	Indels 0;	Gaps 0;

Oy	GACATCCAGATGACCAGATCTCATTCTCCCGTGTGATCTGGTAGAGACAGAGTACC	60
Db	1 GACATCCAGATGACCAGATCTCATTCTCCCGTGTGATCTGGTAGAGACAGAGTACC	60
Oy	ATCACTTGCCGGGCAGTCAGAGCATTTAGACCTTAATTTAAATTGGTATCAGAGAAAACA	120
Db	61 ATCACTTGCCAGGCCGATGAGACAACTTACCACTTTTAAATTGGTATCAGAGAAAACA	120
Oy	GGA CAGCTCTTAAGCTGCTCAATTTACTGGGCATTAACCGGGAGATCCGGGGTCCCTGAC	180
Db	121 GGGAAAGCCCTTAAGCTCTGATCTTACATGATGATCCAATTTGGAAAACGGGGATCCCAATCA	180
Oy	181 CGATTGACGGCAGTGAATCTGGGACAAATTTACACTCTCACCATTCAGCAGGCTCGACCT	240
Db	181 AGGTTTCA GTGAAGTGAATCTGGGACAGATTTTATCTTACACATTCAGGAGCTCTCAACCT	240
Oy	241 GAAGATTTTTGCTTACTTTTGTCAAACGCTGACAGTTTGGCCGATCACTTCGGCCAA	300
Db	241 GAAGATTTTGCACATTTACTGTCAACATTTGATAATCTCCGATCACTTCGGCCAA	300
Oy	301 GGGACACGACTGAGCAATTCAA	321
Db	301 GGGACACGACTGAGCAATTCAA	321

Search completed: September 12, 2005, 02:01:34
Job time : 510.25 secs

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